



## SEQUENCE LISTING

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<120> DIAGNOSIS AND TREATMENT OF MULTIPLE SULFATASE DEFICIENCY AND  
OTHER SULFATASE DEFICIENCIES

<130> 10278-048001

<140> US 10/7<sup>7</sup>5,678

<141> 2004-02-10

<150> US 60/447,747

<151> 2003-02-11

<160> 96

<170> PatentIn version 3.2

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Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr 115 120 125		
Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn 130 135 140		
His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro 145 150 155 160		
Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly 165 170 175		
Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro 180 185 190		
Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu 195 200 205		
Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly 210 215 220		
Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys 225 230 235 240		
Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro 245 250 255		
Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln 260 265 270		
Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile 275 280 285		

Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val  
 290 295 300

Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp  
 305 310 315 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly  
 325 330 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp  
 340 345 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala  
 355 360 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe  
 370 375 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu  
 385 390 395 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu  
 405 410 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys  
 420 425 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu  
 435 440 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser  
 450 455 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro  
 465 470 475 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp  
 485 490 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala  
 500 505 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp  
 515 520 525

Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu  
 530 535 540

Phe Gln Leu Leu Met Pro  
 545 550

<210> 8  
 <211> 2657  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
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 agtggcgcggt acaacaacag cgccatcgcc acccgcacc tggacgcctt ggcccgccgc 180  
 agcctcctct ttcgcaatgc cttcacctcg gtcagcagct gctctcccag ccgcgccagc 240  
 ctctcactg gcttgcccca gcatcagaat gggatgtacg ggctgcacca ggacgtgcac 300  
 cacttcaact ccttcgacaa ggtgcgagc ctgccgctgc tgctcagcca agctggtgtg 360  
 cgcacaggca tcatcgggaa gaagcacgtg gggccggaga ccgtgtaccc gtttgacttt 420  
 gcgtacacgg aggagaatgg ctccgtcctc cagggtggggc ggaacatcac tagaattaag 480  
 ctgctcgtcc ggaaattcct gcagactcag gatgaccggc ctttcttctt ctacgtcgcc 540  
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 tttggcaacg gagagagcgg catgggtcgt atcccagact ggacccccca ggcctacgac 660  
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 gccgctcagt acaccaccgt cggccgcatg gaccaaggag ttggactggt gctccaggag 780  
 ctgcgtgacg ccggtgtcct gaacgacaca ctggtgatct tcacgtccga caacgggatc 840  
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 tcatccccgg agcacccaaa acgctggggc caagtcagcg aggcctacgt gagcctccta 960  
 gacctcacgc ccaccatctt ggattggttc tcgatcccgt accccagcta cgccatcttt 1020  
 ggctcgaaga ccatccacct cactggccgg tccctcctgc cggcgctgga ggccgagccc 1080  
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tattgtaaaa	gctttttt					2657

<210> 9  
 <211> 502  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 9

Met Ser Cys Pro Val Pro Ala Cys Cys Ala Leu Leu Leu Val Leu Gly  
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Leu Cys Arg Ala Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp  
 20 25 30

Gly Gly Phe Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro  
 35 40 45

His Leu Asp Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe  
 50 55 60

Thr Ser Val Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly  
 65 70 75 80

Leu Pro Gln His Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His  
 85 90 95

His Phe Asn Ser Phe Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser  
 100 105 110

Gln Ala Gly Val Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro  
 115 120 125

Glu Thr Val Tyr Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser  
 130 135 140

Val Leu Gln Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg  
 145 150 155 160

Lys Phe Leu Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala  
 165 170 175

Phe His Asp Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr  
 180 185 190

Phe Cys Glu Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro  
 195 200 205

Asp Trp Thr Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr  
 210 215 220

Phe Val Pro Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr  
 225 230 235 240

Thr Thr Val Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu  
 245 250 255

Leu Arg Asp Ala Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser  
 260 265 270

Asp Asn Gly Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro  
 275 280 285

Gly Thr Ala Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg  
 290 295 300

Trp Gly Gln Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro  
 305 310 315 320

Thr Ile Leu Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe  
 325 330 335

Gly Ser Lys Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu  
 340 345 350

Glu Ala Glu Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His  
 355 360 365

Glu Val Thr Met Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe  
 370 375 380

Arg Leu Val His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln  
 385 390 395 400

Asp Phe Tyr Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr  
 405 410 415

Ala Gly Gln Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr  
 420 425 430

Arg Ala Arg Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr  
 435 440 445



Gln Asn Leu Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu  
 450 455 460

Arg Asp Gln Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val  
 465 470 475 480

Cys Ala Pro Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln  
 485 490 495

Pro Leu His Asn Glu Leu  
 500

<210> 10  
 <211> 1014  
 <212> DNA  
 <213> Homo sapiens

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 ccggaaggca gaggttgtag tgagccaaga tcgcgccact gaactccagc ctgggtgaca 120  
 gagtgagact gtctcagaac agcaacaaca aaatgcccgc tgctgctggg tccagaagag 180  
 cttgaataac tgcattgttct ttttctcaat tttcatttcc cagaactggg cacctccggg 240  
 ctgtgaaaag ttaggggaagt gtctgacacc tccagaatcc attcccaaga agtgcctctg 300  
 gtcccactag cacctgcgca gactcaggcc aggcctagaa tctccagttg gccctgcaag 360  
 tgccctggagg aaggatggct ctggcctcgg tcctccccca accctgcca agccagacag 420  
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 gtgtgcttgg ccctcctcct cgcccacggc gcctcagatt tcaggaccct cctcctcgcc 540  
 cacggcgcct cagacctcag gacctgccc tctcacgcct ttgtgaaccc caaatatctg 600  
 agaccagtct cagtttattt tgccaagggt aaggatgcac ctgtgacagc ctcaggaggt 660  
 cctgacaaca ggtgcccag gtggctgggg atacagtttg cttttataca tcttagggag 720  
 acacaagatc agtatgtgta tggcgtacat tggttcagtc agccttcac tgaatacacg 780  
 attgagtctg gccagtgaa tccgcatttt tatgtaaaca gtaagggaac ggggcaatca 840  
 tataagcggt tgtctcagg gagccccaga gggatgactt ccagttccgt ctgtcctttg 900  
 tccacaagga atttccctgg gcgctaatta tgaggaggc gtgtagcttc ttatcattgt 960  
 agctatgtta tttagaaata aaacgggagg caggtttgcc taattcccag gttg 1014

<210> 11  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<400> 11

Met Ala Ala Val Val Ala Ala Thr Arg Trp Trp Gln Leu Leu Leu Val  
 1 5 10 15

Leu Ser Ala Ala Gly Met Gly Ala Ser Gly Ala Pro Gln Pro Pro Asn  
 20 25 30

Ile Leu Leu Leu Leu Met Asp Asp Met Gly Trp Gly Asp Leu Gly Val  
 35 40 45

Tyr Gly Glu Pro Ser Arg Glu Thr Pro Asn Leu Asp Arg Met Ala Ala  
 50 55 60

Glu Gly Leu Leu Phe Pro Asn Phe Tyr Ser Ala Asn Pro Leu Cys Ser  
 65 70 75 80

Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Ile Arg Asn Gly  
 85 90 95

Phe Tyr Thr Thr Asn Ala His Ala Arg Asn Ala Tyr Thr Pro Gln Glu  
 100 105 110

Ile Val Gly Gly Ile Pro Asp Ser Glu Gln Leu Leu Pro Glu Leu Leu  
 115 120 125

Lys Lys Ala Gly Tyr Val Ser Lys Ile Val Gly Lys Trp His Leu Gly  
 130 135 140

His Arg Pro Gln Phe His Pro Leu Lys His Gly Phe Asp Glu Trp Phe  
 145 150 155 160

Gly Ser Pro Asn Cys His Phe Gly Pro Tyr Asp Asn Lys Ala Arg Pro  
 165 170 175

Asn Ile Pro Val Tyr Arg Asp Trp Glu Met Val Gly Arg Tyr Tyr Glu  
 180 185 190

Glu Phe Pro Ile Asn Leu Lys Thr Gly Glu Ala Asn Leu Thr Gln Ile

195		200		205											
Tyr	Leu	Gln	Glu	Ala	Leu	Asp	Phe	Ile	Lys	Arg	Gln	Ala	Arg	His	His
210						215					220				
Pro	Phe	Phe	Leu	Tyr	Trp	Ala	Val	Asp	Ala	Thr	His	Ala	Pro	Val	Tyr
225					230					235					240
Ala	Ser	Lys	Pro	Phe	Leu	Gly	Thr	Ser	Gln	Arg	Gly	Arg	Tyr	Gly	Asp
				245					250					255	
Ala	Val	Arg	Glu	Ile	Asp	Asp	Ser	Ile	Gly	Lys	Ile	Leu	Glu	Leu	Leu
			260					265					270		
Gln	Asp	Leu	His	Val	Ala	Asp	Asn	Thr	Phe	Val	Phe	Phe	Thr	Ser	Asp
	275						280					285			
Asn	Gly	Ala	Ala	Leu	Ile	Ser	Ala	Pro	Glu	Gln	Gly	Gly	Ser	Asn	Gly
290						295					300				
Pro	Phe	Leu	Cys	Gly	Lys	Gln	Thr	Thr	Phe	Glu	Gly	Gly	Met	Arg	Glu
305					310					315					320
Pro	Ala	Leu	Ala	Trp	Trp	Pro	Gly	His	Val	Thr	Ala	Gly	Gln	Val	Ser
				325					330					335	
His	Gln	Leu	Gly	Ser	Ile	Met	Asp	Leu	Phe	Thr	Thr	Ser	Leu	Ala	Leu
		340						345					350		
Ala	Gly	Leu	Thr	Pro	Pro	Ser	Asp	Arg	Ala	Ile	Asp	Gly	Leu	Asn	Leu
	355						360					365			
Leu	Pro	Thr	Leu	Leu	Gln	Gly	Arg	Leu	Met	Asp	Arg	Pro	Ile	Phe	Tyr
370						375					380				
Tyr	Arg	Gly	Asp	Thr	Leu	Met	Ala	Ala	Thr	Leu	Gly	Gln	His	Lys	Ala
385					390					395					400
His	Phe	Trp	Thr	Trp	Thr	Asn	Ser	Trp	Glu	Asn	Phe	Arg	Gln	Gly	Ile
				405					410					415	
Asp	Phe	Cys	Pro	Gly	Gln	Asn	Val	Ser	Gly	Val	Thr	Thr	His	Asn	Leu
			420					425					430		

Glu Asp His Thr Lys Leu Pro Leu Ile Phe His Leu Gly Arg Asp Pro  
 435 440 445

Gly Glu Arg Phe Pro Leu Ser Phe Ala Ser Ala Glu Tyr Gln Glu Ala  
 450 455 460

Leu Ser Arg Ile Thr Ser Val Val Gln Gln His Gln Glu Ala Leu Val  
 465 470 475 480

Pro Ala Gln Pro Gln Leu Asn Val Cys Asn Trp Ala Val Met Asn Trp  
 485 490 495

Ala Pro Pro Gly Cys Glu Lys Leu Gly Lys Cys Leu Thr Pro Pro Glu  
 500 505 510

Ser Ile Pro Lys Lys Cys Leu Trp Ser His  
 515 520

<210> 12  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
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 ccgggggtcac cccggagcct gtccgctatg cggctcctgc ctctagcccc aggtcggctc 120  
 cggcggggca gcccccgcca cctgccctcc tgcagcccag cgctgctact gctggtgctg 180  
 ggcgggtgcc tgggggtctt cgggggtggct gcgggaaccc ggaggcccaa cgtggtgctg 240  
 ctctcacgg acgaccagga cgaagtgtc ggcgcatga caccactaaa gaaaacaaa 300  
 gctctcatcg gagagatggg gatgactttt tccagtgtt atgtgccaag tgctctctgc 360  
 tgccccagca gagccagtat cctgacagga aagtaccac ataatcatca cgttgtgaac 420  
 aacactctgg aggggaactg cagtagtaag tcctggcaga agatccaaga accaaatact 480  
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 tggtagcct tggaaaagaa ttctaagtat tataattaca ccctgtctat caatgggaag 660  
 gcacggaagc atggtgaaaa ctatagtgtg gactacctga cagatgtttt ggctaattgtc 720  
 tccttgagact ttctggacta caagtccaac tttgagcct tttcatgat gatcgccact 780

ccagcgctc attcgcttg gacagctgca cctcagtacc agaaggcttt ccagaatgtc	840
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caagccaaga ctccaatgac taattcttca atacagtttt tagataatgc atttaggaaa	960
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ttcactgggg agctcaacaa cacttacatc ttctatacct cagacaatgg ctatcacaca	1080
ggacagtttt ccttgccaat agacaagaga cagctgtatg agtttgatat caaagttcca	1140
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gatgggatgt ccttattgcc cattttgaga ggtgccagta acttgacctg gcgatcagat	1320
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agtctggcg tatctcaatg cttcccagac tgtgtatgtg aagatgctta taacaatacc	1440
tatgcctgtg tgaggacaat gtcagcattg tggaatttgc agtattgcga gtttgatgac	1500
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tcctgttctg ggccaacctg tcgcactcca ggggtttttg accccggata caggtttgac	1680
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gattgtagta ggtgtctgta gctagtcttc aagaccacac ctggaagagt ttctgggctg	1860
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gcttgaagag taaccatcag agctgaatca tccaagtaag aacaagtacc attgttgatt	2280
gataagtaga gatacatctt ttatgatgtt catcacagtg tggttaagggtt gcaaattcaa	2340
aacatgtcac ccaagctctg ttcattgttt tgtgaattc	2379

<211> 552  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met Arg Leu Leu Pro Leu Ala Pro Gly Arg Leu Arg Arg Gly Ser Pro  
 1 5 10 15

Arg His Leu Pro Ser Cys Ser Pro Ala Leu Leu Leu Leu Val Leu Gly  
 20 25 30

Gly Cys Leu Gly Val Phe Gly Val Ala Ala Gly Thr Arg Arg Pro Asn  
 35 40 45

Val Val Leu Leu Leu Thr Asp Asp Gln Asp Glu Val Leu Gly Gly Met  
 50 55 60

Thr Pro Leu Lys Lys Thr Lys Ala Leu Ile Gly Glu Met Gly Met Thr  
 65 70 75 80

Phe Ser Ser Ala Tyr Val Pro Ser Ala Leu Cys Cys Pro Ser Arg Ala  
 85 90 95

Ser Ile Leu Thr Gly Lys Tyr Pro His Asn His His Val Val Asn Asn  
 100 105 110

Thr Leu Glu Gly Asn Cys Ser Ser Lys Ser Trp Gln Lys Ile Gln Glu  
 115 120 125

Pro Asn Thr Phe Pro Ala Ile Leu Arg Ser Met Cys Gly Tyr Gln Thr  
 130 135 140

Phe Phe Ala Gly Lys Tyr Leu Asn Glu Tyr Gly Ala Pro Asp Ala Gly  
 145 150 155 160

Gly Leu Glu His Val Pro Leu Gly Trp Ser Tyr Trp Tyr Ala Leu Glu  
 165 170 175

Lys Asn Ser Lys Tyr Tyr Asn Tyr Thr Leu Ser Ile Asn Gly Lys Ala  
 180 185 190

Arg Lys His Gly Glu Asn Tyr Ser Val Asp Tyr Leu Thr Asp Val Leu  
 195 200 205

Ala Asn Val Ser Leu Asp Phe Leu Asp Tyr Lys Ser Asn Phe Glu Pro  
 210 215 220

Phe Phe Met Met Ile Ala Thr Pro Ala Pro His Ser Pro Trp Thr Ala  
 225 230 235 240

Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val Phe Ala Pro Arg Asn  
 245 250 255

Lys Asn Phe Asn Ile His Gly Thr Asn Lys His Trp Leu Ile Arg Gln  
 260 265 270

Ala Lys Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala  
 275 280 285

Phe Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu  
 290 295 300

Lys Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr  
 305 310 315 320

Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln Phe Ser Leu  
 325 330 335

Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys Val Pro Leu  
 340 345 350

Leu Val Arg Gly Pro Gly Ile Lys Pro Asn Gln Thr Ser Lys Met Leu  
 355 360 365

Val Ala Asn Ile Asp Leu Gly Pro Thr Ile Leu Asp Ile Ala Gly Tyr  
 370 375 380

Asp Leu Asn Lys Thr Gln Met Asp Gly Met Ser Leu Leu Pro Ile Leu  
 385 390 395 400

Arg Gly Ala Ser Asn Leu Thr Trp Arg Ser Asp Val Leu Val Glu Tyr  
 405 410 415

Gln Gly Glu Gly Arg Asn Val Thr Asp Pro Thr Cys Pro Ser Leu Ser  
 420 425 430

Pro Gly Val Ser Gln Cys Phe Pro Asp Cys Val Cys Glu Asp Ala Tyr  
 435 440 445

Asn Asn Thr Tyr Ala Cys Val Arg Thr Met Ser Ala Leu Trp Asn Leu  
 450 455 460

Gln Tyr Cys Glu Phe Asp Asp Gln Glu Val Phe Val Glu Val Tyr Asn  
 465 470 475 480

Leu Thr Ala Asp Pro Asp Gln Ile Thr Asn Ile Ala Lys Thr Ile Asp  
 485 490 495

Pro Glu Leu Leu Gly Lys Met Asn Tyr Arg Leu Met Met Leu Gln Ser  
 500 505 510

Cys Ser Gly Pro Thr Cys Arg Thr Pro Gly Val Phe Asp Pro Gly Tyr  
 515 520 525

Arg Phe Asp Pro Arg Leu Met Phe Ser Asn Arg Gly Ser Val Arg Thr  
 530 535 540

Arg Arg Phe Ser Lys His Leu Leu  
 545 550

<210> 14  
 <211> 2022  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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 agcgccaagt gacttacgcc cccgaccctg agcccggacc gctaggcgag gaggatcaga 120  
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<210> 15
<211> 507
<212> PRT
<213> Homo sapiens

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<400> 15

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Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn  
35 40 45

Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val  
50 55 60

Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg  
65 70 75 80

Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser  
85 90 95

Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala  
100 105 110

Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val  
115 120 125

Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe  
130 135 140

Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr  
145 150 155 160

Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu  
165 170 175

Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro  
180 185 190

Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu  
195 200 205

Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala  
210 215 220

Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu

225		230		235		240
Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala						
		245		250		255
Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu						
		260		265		270
Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg						
		275		280		285
Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr						
		290		295		300
Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly						
305		310		315		320
His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu						
		325		330		335
Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr						
		340		345		350
Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser						
		355		360		365
Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg						
		370		375		380
Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr						
385		390		395		400
Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala						
		405		410		415
Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser						
		420		425		430
Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala						
		435		440		445
Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala						
		450		455		460

Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly  
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Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg  
 485 490 495

Pro Ala Cys Cys His Cys Pro Asp Pro His Ala  
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<210> 16  
 <211> 2228  
 <212> DNA  
 <213> Homo sapiens

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<210> 17
<211> 533
<212> PRT
<213> Homo sapiens

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<400> 17
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Met Gly Pro Arg Gly Ala Ala Ser Leu Pro Arg Gly Pro Gly Pro Arg
1           5           10           15

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Arg Leu Leu Leu Pro Val Val Leu Pro Leu Leu Leu Leu Leu Leu
20           25           30

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Ala Pro Pro Gly Ser Gly Ala Gly Ala Ser Arg Pro Pro His Leu Val
35           40           45

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Phe Leu Leu Ala Asp Asp Leu Gly Trp Asn Asp Val Gly Phe His Gly  
 50 55 60

Ser Arg Ile Arg Thr Pro His Leu Asp Ala Leu Ala Ala Gly Gly Val  
 65 70 75 80

Leu Leu Asp Asn Tyr Tyr Thr Gln Pro Leu Cys Thr Pro Ser Arg Ser  
 85 90 95

Gln Leu Leu Thr Gly Arg Tyr Gln Ile Arg Thr Gly Leu Gln His Gln  
 100 105 110

Ile Ile Trp Pro Cys Gln Pro Ser Cys Val Pro Leu Asp Glu Lys Leu  
 115 120 125

Leu Pro Gln Leu Leu Lys Glu Ala Gly Tyr Thr Thr His Met Val Gly  
 130 135 140

Lys Trp His Leu Gly Met Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg  
 145 150 155 160

Gly Phe Asp Thr Tyr Phe Gly Tyr Leu Leu Gly Ser Glu Asp Tyr Tyr  
 165 170 175

Ser His Glu Arg Cys Thr Leu Ile Asp Ala Leu Asn Val Thr Arg Cys  
 180 185 190

Ala Leu Asp Phe Arg Asp Gly Glu Glu Val Ala Thr Gly Tyr Lys Asn  
 195 200 205

Met Tyr Ser Thr Asn Ile Phe Thr Lys Arg Ala Ile Ala Leu Ile Thr  
 210 215 220

Asn His Pro Pro Glu Lys Pro Leu Phe Leu Tyr Leu Ala Leu Gln Ser  
 225 230 235 240

Val His Glu Pro Leu Gln Val Pro Glu Glu Tyr Leu Lys Pro Tyr Asp  
 245 250 255

Phe Ile Gln Asp Lys Asn Arg His His Tyr Ala Gly Met Val Ser Leu  
 260 265 270

Met Asp Glu Ala Val Gly Asn Val Thr Ala Ala Leu Lys Ser Ser Gly  
 275 280 285

Leu Trp Asn Asn Thr Val Phe Ile Phe Ser Thr Asp Asn Gly Gly Gln  
 290 295 300

Thr Leu Ala Gly Gly Asn Asn Trp Pro Leu Arg Gly Arg Lys Trp Ser  
 305 310 315 320

Leu Trp Glu Gly Gly Val Arg Gly Val Gly Phe Val Ala Ser Pro Leu  
 325 330 335

Leu Lys Gln Lys Gly Val Lys Asn Arg Glu Leu Ile His Ile Ser Asp  
 340 345 350

Trp Leu Pro Thr Leu Val Lys Leu Ala Arg Gly His Thr Asn Gly Thr  
 355 360 365

Lys Pro Leu Asp Gly Phe Asp Val Trp Lys Thr Ile Ser Glu Gly Ser  
 370 375 380

Pro Ser Pro Arg Ile Glu Leu Leu His Asn Ile Asp Pro Asn Phe Val  
 385 390 395 400

Asp Ser Ser Pro Cys Pro Arg Asn Ser Met Ala Pro Ala Lys Asp Asp  
 405 410 415

Ser Ser Leu Pro Glu Tyr Ser Ala Phe Asn Thr Ser Val His Ala Ala  
 420 425 430

Ile Arg His Gly Asn Trp Lys Leu Leu Thr Gly Tyr Pro Gly Cys Gly  
 435 440 445

Tyr Trp Phe Pro Pro Pro Ser Gln Tyr Asn Val Ser Glu Ile Pro Ser  
 450 455 460

Ser Asp Pro Pro Thr Lys Thr Leu Trp Leu Phe Asp Ile Asp Arg Asp  
 465 470 475 480

Pro Glu Glu Arg His Asp Leu Ser Arg Glu Tyr Pro His Ile Val Thr  
 485 490 495

Lys Leu Leu Ser Arg Leu Gln Phe Tyr His Lys His Ser Val Pro Val  
 500 505 510

Tyr Phe Pro Ala Gln Asp Pro Arg Cys Asp Pro Lys Ala Thr Gly Val  
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Trp Gly Pro Trp Met  
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<210> 18  
 <211> 2401  
 <212> DNA  
 <213> Homo sapiens

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<210> 19
<211> 583
<212> PRT
<213> Homo sapiens

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<400> 19
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Met Pro Leu Arg Lys Met Lys Ile Pro Phe Leu Leu Leu Phe Phe Leu
1           5           10           15

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Trp Glu Ala Glu Ser His Ala Ala Ser Arg Pro Asn Ile Ile Leu Val
          20           25           30

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Met Ala Asp Asp Leu Gly Ile Gly Asp Pro Gly Cys Tyr Gly Asn Lys  
 35 40 45

Thr Ile Arg Thr Pro Asn Ile Asp Arg Leu Ala Ser Gly Gly Val Lys  
 50 55 60

Leu Thr Gln His Leu Ala Ala Ser Pro Leu Cys Thr Pro Ser Arg Ala  
 65 70 75 80

Ala Phe Met Thr Gly Arg Tyr Pro Val Arg Ser Gly Met Ala Ser Trp  
 85 90 95

Ser Arg Thr Gly Val Phe Leu Phe Thr Ala Ser Ser Gly Gly Leu Pro  
 100 105 110

Thr Asp Glu Ile Thr Phe Ala Lys Leu Leu Lys Asp Gln Gly Tyr Ser  
 115 120 125

Thr Ala Leu Ile Gly Lys Trp His Leu Gly Met Ser Cys His Ser Lys  
 130 135 140

Thr Asp Phe Cys His His Pro Leu His His Gly Phe Asn Tyr Phe Tyr  
 145 150 155 160

Gly Ile Ser Leu Thr Asn Leu Arg Asp Cys Lys Pro Gly Glu Gly Ser  
 165 170 175

Val Phe Thr Thr Gly Phe Lys Arg Leu Val Phe Leu Pro Leu Gln Ile  
 180 185 190

Val Gly Val Thr Leu Leu Thr Leu Ala Ala Leu Asn Cys Leu Gly Leu  
 195 200 205

Leu His Val Pro Leu Gly Val Phe Phe Ser Leu Leu Phe Leu Ala Ala  
 210 215 220

Leu Ile Leu Thr Leu Phe Leu Gly Phe Leu His Tyr Phe Arg Pro Leu  
 225 230 235 240

Asn Cys Phe Met Met Arg Asn Tyr Glu Ile Ile Gln Gln Pro Met Ser  
 245 250 255

Tyr Asp Asn Leu Thr Gln Arg Leu Thr Val Glu Ala Ala Gln Phe Ile  
 260 265 270

Gln Arg Asn Thr Glu Thr Pro Phe Leu Leu Val Leu Ser Tyr Leu His  
 275 280 285

Val His Thr Ala Leu Phe Ser Ser Lys Asp Phe Ala Gly Lys Ser Gln  
 290 295 300

His Gly Val Tyr Gly Asp Ala Val Glu Glu Met Asp Trp Ser Val Gly  
 305 310 315 320

Gln Ile Leu Asn Leu Leu Asp Glu Leu Arg Leu Ala Asn Asp Thr Leu  
 325 330 335

Ile Tyr Phe Thr Ser Asp Gln Gly Ala His Val Glu Glu Val Ser Ser  
 340 345 350

Lys Gly Glu Ile His Gly Gly Ser Asn Gly Ile Tyr Lys Gly Gly Lys  
 355 360 365

Ala Asn Asn Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Leu Arg Trp  
 370 375 380

Pro Arg Val Ile Gln Ala Gly Gln Lys Ile Asp Glu Pro Thr Ser Asn  
 385 390 395 400

Met Asp Ile Phe Pro Thr Val Ala Lys Leu Ala Gly Ala Pro Leu Pro  
 405 410 415

Glu Asp Arg Ile Ile Asp Gly Arg Asp Leu Met Pro Leu Leu Glu Gly  
 420 425 430

Lys Ser Gln Arg Ser Asp His Glu Phe Leu Phe His Tyr Cys Asn Ala  
 435 440 445

Tyr Leu Asn Ala Val Arg Trp His Pro Gln Asn Ser Thr Ser Ile Trp  
 450 455 460

Lys Ala Phe Phe Phe Thr Pro Asn Phe Asn Pro Val Gly Ser Asn Gly  
 465 470 475 480

Cys Phe Ala Thr His Val Cys Phe Cys Phe Gly Ser Tyr Val Thr His  
485 490 495

His Asp Pro Pro Leu Leu Phe Asp Ile Ser Lys Asp Pro Arg Glu Arg  
500 505 510

Asn Pro Leu Thr Pro Ala Ser Glu Pro Arg Phe Tyr Glu Ile Leu Lys  
515 520 525

Val Met Gln Glu Ala Ala Asp Arg His Thr Gln Thr Leu Pro Glu Val  
530 535 540

Pro Asp Gln Phe Ser Trp Asn Asn Phe Leu Trp Lys Pro Trp Leu Gln  
545 550 555 560

Leu Cys Cys Pro Ser Thr Gly Leu Ser Cys Gln Cys Asp Arg Glu Lys  
565 570 575

Gln Asp Lys Arg Leu Ser Arg  
580

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<210> 20
<211> 1945
<212> DNA
<213> Homo sapiens
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gctctttgac ctctccaggg acccctccga ggcacggccc ctgacccccg actccgagcc    1680
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gtgctgcgga catttcccgt tctgttcatg ccacaggat ggggatggca cccctgaat    1860
gccaggactg tgagagagga tccaggagag cctgactgcg ttgcaaacia aattctccaa    1920
gcttggttct atcttcagtc cggaa                                           1945

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```

<210> 21
<211> 593
<212> PRT
<213> Homo sapiens

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<400> 21
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Met Arg Ser Ala Ala Arg Arg Gly Arg Ala Ala Pro Ala Ala Arg Asp
1           5           10           15

```

```

Ser Leu Pro Val Leu Leu Phe Leu Cys Leu Leu Leu Lys Thr Cys Glu
      20           25           30

```

Pro Lys Thr Ala Asn Ala Phe Lys Pro Asn Ile Leu Leu Ile Met Ala  
 35 40 45

Asp Asp Leu Gly Thr Gly Asp Leu Gly Cys Tyr Gly Asn Asn Thr Leu  
 50 55 60

Arg Thr Pro Asn Ile Asp Gln Leu Ala Glu Glu Gly Val Arg Leu Thr  
 65 70 75 80

Gln His Leu Ala Ala Ala Pro Leu Cys Thr Pro Ser Arg Ala Ala Phe  
 85 90 95

Leu Thr Gly Arg His Ser Phe Arg Ser Gly Met Asp Ala Ser Asn Gly  
 100 105 110

Tyr Arg Ala Leu Gln Trp Asn Ala Gly Ser Gly Gly Leu Pro Glu Asn  
 115 120 125

Glu Thr Thr Phe Ala Arg Ile Leu Gln Gln His Gly Tyr Ala Thr Gly  
 130 135 140

Leu Ile Gly Lys Trp His Gln Gly Val Asn Cys Ala Ser Arg Gly Asp  
 145 150 155 160

His Cys His His Pro Leu Asn His Gly Phe Asp Tyr Phe Tyr Gly Met  
 165 170 175

Pro Phe Thr Leu Thr Asn Asp Cys Asp Pro Gly Arg Pro Pro Glu Val  
 180 185 190

Asp Ala Ala Leu Arg Ala Gln Leu Trp Gly Tyr Thr Gln Phe Leu Ala  
 195 200 205

Leu Gly Ile Leu Thr Leu Ala Ala Gly Gln Thr Cys Gly Phe Phe Ser  
 210 215 220

Val Ser Ala Arg Ala Val Thr Gly Met Ala Gly Val Gly Cys Leu Phe  
 225 230 235 240

Phe Ile Ser Trp Tyr Ser Ser Phe Gly Phe Val Arg Arg Trp Asn Cys  
 245 250 255

Ile Leu Met Arg Asn His Asp Val Thr Glu Gln Pro Met Val Leu Glu  
 260 265 270

Lys Thr Ala Ser Leu Met Leu Lys Glu Ala Val Ser Tyr Ile Glu Arg  
 275 280 285

His Lys His Gly Pro Phe Leu Leu Phe Leu Ser Leu Leu His Val His  
 290 295 300

Ile Pro Leu Val Thr Thr Ser Ala Phe Leu Gly Lys Ser Gln His Gly  
 305 310 315 320

Leu Tyr Gly Asp Asn Val Glu Glu Met Asp Trp Leu Ile Gly Lys Val  
 325 330 335

Leu Asn Ala Ile Glu Asp Asn Gly Leu Lys Asn Ser Thr Phe Thr Tyr  
 340 345 350

Phe Thr Ser Asp His Gly Gly His Leu Glu Ala Arg Asp Gly His Ser  
 355 360 365

Gln Leu Gly Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly  
 370 375 380

Gly Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Phe His Trp Pro Gly  
 385 390 395 400

Val Leu Pro Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp  
 405 410 415

Val Phe Pro Thr Val Val Gln Leu Val Gly Gly Glu Val Pro Gln Asp  
 420 425 430

Arg Val Ile Asp Gly His Ser Leu Val Pro Leu Leu Gln Gly Ala Glu  
 435 440 445

Ala Arg Ser Ala His Glu Phe Leu Phe His Tyr Cys Gly Gln His Leu  
 450 455 460

His Ala Ala Arg Trp His Gln Lys Asp Ser Gly Ser Val Trp Lys Val  
 465 470 475 480

His Tyr Thr Thr Pro Gln Phe His Pro Glu Glu Arg Gly Leu Leu Thr  
 485 490 495

Ala Glu Ala Ser Ala His Ala Glu Trp Gly Gly Val Thr His His Arg  
 500 505 510

Pro Pro Leu Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Ala Arg Pro  
 515 520 525

Leu Thr Pro Asp Ser Glu Pro Leu Tyr His Ala Val Ile Ala Arg Val  
 530 535 540

Gly Ala Ala Val Ser Glu His Arg Gln Thr Leu Ser Pro Val Pro Gln  
 545 550 555 560

Gln Phe Ser Met Ser Asn Ile Leu Trp Lys Pro Trp Leu Gln Pro Cys  
 565 570 575

Cys Gly His Phe Pro Phe Cys Ser Cys His Glu Asp Gly Asp Gly Thr  
 580 585 590

Pro

<210> 22  
 <211> 1858  
 <212> DNA  
 <213> Homo sapiens

<400> 22  
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 gctcgctgta ctgctaagtt tggcaccatc agcttccagc gacatttccg cctcccgacc 180  
 gaacatcctt cttctgatgg cggacgacct tggcattggg gacattggct gctatggcaa 240  
 caacaccatg aggactccga atattgaccg ccttgcagag gacggcgtga agctgaccca 300  
 acacatctct gccgcatctt tgtgcacccc aagcagagcc gccttctca cgggcagata 360  
 ccctgtgcga tcagggatgg tttccagcat tggttaccgt gttcttcagt ggaccggagc 420  
 atctggaggt cttccaacaa atgagacaac ttttgcaaaa atactgaaag agaaaggcta 480  
 tgccactgga ctcatggaa aatggcatct gggctctcaac tgtgagtcag ccagtgatca 540  
 ttgccaccac cctctccatc atggctttga gcatttctac ggaatgcctt tctccttgat 600



```

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```

<210> 23
<211> 589
<212> PRT
<213> Homo sapiens

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<400> 23
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```

Met Leu His Leu His His Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
1           5           10          15

```

```

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
20           25           30

```

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu  
           35                                  40                                  45

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro  
       50                                  55                                  60

Asn Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile  
   65                                  70                                  75                                  80

Ser Ala Ala Ser Leu Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly  
                                   85                                  90                                  95

Arg Tyr Pro Val Arg Ser Gly Met Val Ser Ser Ile Gly Tyr Arg Val  
                                   100                                  105                                  110

Leu Gln Trp Thr Gly Ala Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr  
                                   115                                  120                                  125

Phe Ala Lys Ile Leu Lys Glu Lys Gly Tyr Ala Thr Gly Leu Ile Gly  
       130                                  135                                  140

Lys Trp His Leu Gly Leu Asn Cys Glu Ser Ala Ser Asp His Cys His  
   145                                  150                                  155                                  160

His Pro Leu His His Gly Phe Glu His Phe Tyr Gly Met Pro Phe Ser  
                                   165                                  170                                  175

Leu Met Gly Asp Cys Ala Arg Trp Glu Leu Ser Glu Lys Arg Val Asn  
                                   180                                  185                                  190

Leu Glu Gln Lys Leu Asn Phe Leu Phe Gln Val Leu Ala Leu Val Ala  
                                   195                                  200                                  205

Leu Thr Leu Val Ala Gly Lys Leu Thr His Leu Ile Pro Val Ser Trp  
       210                                  215                                  220

Met Pro Val Ile Trp Ser Ala Leu Ser Ala Val Leu Leu Leu Ala Ser  
   225                                  230                                  235                                  240

Ser Tyr Phe Val Gly Ala Leu Ile Val His Ala Asp Cys Phe Leu Met  
                                   245                                  250                                  255

Arg Asn His Thr Ile Thr Glu Gln Pro Met Cys Phe Gln Arg Thr Thr  
 260 265 270

Pro Leu Ile Leu Gln Glu Val Ala Ser Phe Leu Lys Arg Asn Lys His  
 275 280 285

Gly Pro Phe Leu Leu Phe Val Ser Phe Leu His Val His Ile Pro Leu  
 290 295 300

Ile Thr Met Glu Asn Phe Leu Gly Lys Ser Leu His Gly Leu Tyr Gly  
 305 310 315 320

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Arg Ile Leu Asp Thr  
 325 330 335

Leu Asp Val Glu Gly Leu Ser Asn Ser Thr Leu Ile Tyr Phe Thr Ser  
 340 345 350

Asp His Gly Gly Ser Leu Glu Asn Gln Leu Gly Asn Thr Gln Tyr Gly  
 355 360 365

Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu  
 370 375 380

Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Gly Val Leu Pro  
 385 390 395 400

Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp Val Phe Pro  
 405 410 415

Thr Val Val Arg Leu Ala Gly Gly Glu Val Pro Gln Asp Arg Val Ile  
 420 425 430

Asp Gly Gln Asp Leu Leu Pro Leu Leu Leu Gly Thr Ala Gln His Ser  
 435 440 445

Asp His Glu Phe Leu Met His Tyr Cys Glu Arg Phe Leu His Ala Ala  
 450 455 460

Arg Trp His Gln Arg Asp Arg Gly Thr Met Trp Lys Val His Phe Val  
 465 470 475 480

Thr Pro Val Phe Gln Pro Glu Gly Ala Gly Ala Cys Tyr Gly Arg Lys  
                   485                  490                  495

Val Cys Pro Cys Phe Gly Glu Lys Val Val His His Asp Pro Pro Leu  
                   500                  505                  510

Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Thr His Ile Leu Thr Pro  
                   515                  520                  525

Ala Ser Glu Pro Val Phe Tyr Gln Val Met Glu Arg Val Gln Gln Ala  
                   530                  535                  540

Val Trp Glu His Gln Arg Thr Leu Ser Pro Val Pro Leu Gln Leu Asp  
                   545                  550                  555                  560

Arg Leu Gly Asn Ile Trp Arg Pro Trp Leu Gln Pro Cys Cys Gly Pro  
                   565                  570                  575

Phe Pro Leu Cys Trp Cys Leu Arg Glu Asp Asp Pro Gln  
                   580                  585

<210> 24  
 <211> 1996  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
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 gaacacatgg ccagggcaca cagggatgcat gacgacaagg cctaataattg tcctaatacat 180  
 ggttgatgac ctgggtattg gagatctggg ctgctacggc aatgacacca tgaggacgcc 240  
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 ttatgggttt gactactact atggcatgcc gttcactctc gttgacagct gctggccgga 600  
 cccctctcgt aacacggaat tagcctttga gagtcagctc tggctctgtg tgcagctagt 660  
 tgccattgcc atcctcacc taacctttgg gaagctgagc ggctgggtct ctgttcctg 720

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gcccataaag gctgaacgag ctggatccat tatggtgaag gaagcgattt cctttttaga 900
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ccccaccacg gacgatttca ctggcaccag caagcatggc ttgtatgggg ataatgtgga 1020
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ccagaggaag cctttggtcc taacgagaag agataattac aatcaggcta ccaaaggaag 1920
cactaacttt ggtgctttca agttggcaag gagtgcattt aatagtcaat aaattcatct 1980
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<210> 25
<211> 591
<212> PRT
<213> Homo sapiens

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<400> 25

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Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys Ala Leu
1          5          10          15

```

Leu Asn Thr Trp Pro Gly His Thr Gly Cys Met Thr Thr Arg Pro Asn  
 20 25 30

Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly Cys  
 35 40 45

Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala Arg  
 50 55 60

Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys Ser  
 65 70 75 80

Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser Gly  
 85 90 95

Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val Pro  
 100 105 110

Ala Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Ala Leu Leu Lys Lys  
 115 120 125

Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu Asn  
 130 135 140

Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly Phe  
 145 150 155 160

Asp Tyr Tyr Tyr Gly Met Pro Phe Thr Leu Val Asp Ser Cys Trp Pro  
 165 170 175

Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp Leu  
 180 185 190

Cys Val Gln Leu Val Ala Ile Ala Ile Leu Thr Leu Thr Phe Gly Lys  
 195 200 205

Leu Ser Gly Trp Val Ser Val Pro Trp Leu Leu Ile Phe Ser Met Ile  
 210 215 220

Leu Phe Ile Phe Leu Leu Gly Tyr Ala Trp Phe Ser Ser His Thr Ser  
 225 230 235 240

Pro Leu Tyr Trp Asp Cys Leu Leu Met Arg Gly His Glu Ile Thr Glu

	245		250		255
Gln Pro Met Lys Ala Glu Arg Ala Gly Ser Ile Met Val Lys Glu Ala	260		265		270
Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe Phe	275		280		285
Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe Thr	290		295		300
Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met Asp	305		310		315
Ser Met Val Gly Lys Ile Leu Asp Ala Ile Asp Asp Phe Gly Leu Arg	325		330		335
Asn Asn Thr Leu Val Tyr Phe Thr Ser Asp His Gly Gly His Leu Glu	340		345		350
Ala Arg Arg Gly His Ala Gln Leu Gly Gly Trp Asn Gly Ile Tyr Lys	355		360		365
Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro Gly	370		375		380
Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys Glu	385		390		395
Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser Gly	405		410		415
Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met Pro	420		425		430
Leu Leu Gln Gly Asn Val Arg His Ser Glu His Glu Phe Leu Phe His	435		440		445
Tyr Cys Gly Ser Tyr Leu His Ala Val Arg Trp Ile Pro Lys Asp Asp	450		455		460
Ser Gly Ser Val Trp Lys Ala His Tyr Val Thr Pro Val Phe Gln Pro	465		470		475
					480

Pro Ala Ser Gly Gly Cys Tyr Val Thr Ser Leu Cys Arg Cys Phe Gly  
485 490 495

Glu Gln Val Thr Tyr His Asn Pro Pro Leu Leu Phe Asp Leu Ser Arg  
500 505 510

Asp Pro Ser Glu Ser Thr Pro Leu Thr Pro Ala Thr Glu Pro Leu Tyr  
515 520 525

Asp Phe Val Ile Lys Lys Val Ala Asn Ala Leu Lys Glu His Gln Glu  
530 535 540

Thr Ile Val Pro Val Thr Tyr Gln Leu Ser Glu Leu Asn Gln Gly Arg  
545 550 555 560

Thr Trp Leu Lys Pro Cys Cys Gly Val Phe Pro Phe Cys Leu Cys Asp  
565 570 575

Lys Glu Glu Glu Val Ser Gln Pro Arg Gly Pro Asn Glu Lys Arg  
580 585 590

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<210> 26
<211> 1578
<212> DNA
<213> Homo sapiens
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actgccaa	ttgataagat	ggcttcggag	ggaatgaggt	ttgtggattt	ccatgcagct		240
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ctccctcttt	atgaaaacct	caacattgtg	gagcagccgg	tgaacttgag	cagccttgcc		660



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gaggtcagaa aggttcttgc agacgtcctc caagacattg ccaacgacaa catctccagc 1500
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cgctgtcaag ccgcataa 1578

```

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<210> 27
<211> 525
<212> PRT
<213> Homo sapiens

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<400> 27

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```

Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser Phe Ser
1           5           10          15

```

```

Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
          20           25          30

```

```

Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
          35           40          45

```

```

Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
          50           55          60

```

Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala  
65 70 75 80

Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu  
85 90 95

Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly  
100 105 110

Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala  
115 120 125

Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly  
130 135 140

Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro  
145 150 155 160

Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro  
165 170 175

Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln  
180 185 190

Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn  
195 200 205

Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala  
210 215 220

Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro  
225 230 235 240

Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val  
245 250 255

Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly  
260 265 270

Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp  
275 280 285

His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly

290	295	300
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Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr 325 330 335		
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Ser	Ser	Pro	Ser	Trp	Gln	Ala	Met	His	Glu	Pro	Arg	Thr	Phe	Ala	Val	115	120	125	
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Gly	Ile	Lys	Glu	Lys	His	Gly	Phe	Asp	Tyr	Ala	Lys	Asp	Tyr	Phe	Thr	180	185	190	
Asp	Leu	Ile	Thr	Asn	Glu	Ser	Ile	Asn	Tyr	Phe	Lys	Met	Ser	Lys	Arg	195	200	205	
Met	Tyr	Pro	His	Arg	Pro	Val	Met	Met	Val	Ile	Ser	His	Ala	Ala	Pro	210	215	220	

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Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met  
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Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser  
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Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala  
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Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile



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<212> DNA

<213> Homo sapiens

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<400> 31
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Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
1          5          10          15

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Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Leu Lys
          20          25          30

```

```

Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu
          35          40          45

```

```

Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met
          50          55          60

```

```

Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Ala His Phe Ile Asn
65          70          75          80

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Ala Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu  
85 90 95

Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn  
100 105 110

Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala  
115 120 125

Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr  
130 135 140

Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp  
145 150 155 160

Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg  
165 170 175

Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu  
180 185 190

Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys  
195 200 205

Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala  
210 215 220

Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro  
225 230 235 240

Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro  
245 250 255

Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His  
260 265 270

Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met  
275 280 285

Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr  
290 295 300

Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr

305		310		315		320
His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu						
		325		330		335
Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala						
		340		345		350
Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr						
		355		360		365
Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys						
		370		375		380
Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His						
		385		390		395
						400
Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg						
		405		410		415
Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu						
		420		425		430
Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg						
		435		440		445
Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys						
		450		455		460
Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro						
		465		470		475
						480
Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr						
		485		490		495
Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys						
		500		505		510
Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys						
		515		520		525
Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val						
		530		535		540

Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg  
 545 550 555 560

Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp  
 565 570 575

Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser  
 580 585 590

Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn  
 595 600 605

Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp  
 610 615 620

Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn  
 625 630 635 640

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg  
 645 650 655

Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys  
 660 665 670

Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly  
 675 680 685

Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys  
 690 695 700

Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys  
 705 710 715 720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln  
 725 730 735

Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala  
 740 745 750

Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn  
 755 760 765



Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu  
 770 775 780

Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg  
 785 790 795 800

Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys  
 805 810 815

Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly  
 820 825 830

Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg  
 835 840 845

Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu  
 850 855 860

Trp Glu Gly Trp Glu Gly  
 865 870

<210> 32  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<220>  
 <221> VARIANT  
 <222> 1  
 <223> Leu or Val

<220>  
 <221> VARIANT  
 <222> 2  
 <223> Cys or Ser

<220>  
 <221> misc\_feature  
 <222> 3  
 <223> Xaa can be any naturally occurring amino acid

<400> 32

Xaa Xaa Xaa Pro Ser Arg  
 1 5

<210> 33  
 <211> 23  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Sequence derived from human Arylsulfatase A

<400> 33

Met Thr Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala  
 1 5 10 15

Ala Leu Leu Thr Gly Arg Ser  
 20

<210> 34  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> a variant of the ASA65-80 peptide, in which residues Cys69, Pro71 and Arg73, critical for FGly formation, were scrambled

<400> 34

Pro Val Ser Leu Pro Thr Arg Ser Cys Ala Ala Leu Leu Thr Gly Arg  
 1 5 10 15

<210> 35  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> a variant of the ASA65-80 peptide, in which the Cys69 was replaced by a Serine

<400> 35

Pro Val Ser Leu Ser Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg  
 1 5 10 15

<210> 36  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> human FGE-specific PCR primer

<400> 36  
ccaatgtagg tcagacacg 19

<210> 37  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> human FGE-specific PCR primer

<400> 37  
acatggcccg cgggac 16

<210> 38  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> human FGE-specific PCR primer

<400> 38  
cgactgctcc ttggactgg 19

<210> 39  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> human FGE-specific PCR primer

<400> 39  
ggaattcggg acaacatggc tgcg 24

<210> 40  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> HA-specific primer

<400> 40  
cccaagctta tgcgtagtca ggcacatcat acggatagtc catggtgggc aggc 54

<210> 41  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>

<223> c-myc -specific primer

<400> 41

cccaagctta caggtcttct tcagaaatca gcttttggtc gtccatggtg ggcaggc 57

<210> 42

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> RGS-His6 - specific primer

<400> 42

cccaagctta gtgatggtga tggatgatgcg atcctctgtc catggtgggc aggc 54

<210> 43

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> tryptic oligopeptide from a human FGE preparation

<400> 43

Ser	Gln	Asn	Thr	Pro	Asp	Ser	Ser	Ala	Ser	Asn	Leu	Gly	Phe	Arg
1				5				10					15	

<210> 44

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> tryptic oligopeptide from a human FGE preparation

<220>

<221> MISC\_FEATURE

<222> (1)..(19)

<223> tryptic oligopeptide from a human FGE preparation

<400> 44

Met	Val	Pro	Ile	Pro	Ala	Gly	Val	Phe	Thr	Met	Gly	Thr	Asp	Asp	Pro
1				5				10					15		

Gln Ile Lys

<210> 45  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

<400> 45  
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 aagctaggaa atggacaggc tactagcatg gtccaactgc aggggtgggag attcctgatg 120  
 ggaacaaatt ctccagacag cagagatggt gaagggcctg tgcgggaggc gacagtgaaa 180  
 cccttttgcca tcgacatatt tcctgtcacc aacaaagatt tcagggattt tgtcagggag 240  
 aaaaagtatc ggacagaagc tgagatgttt ggatggagct ttgtctttga ggactttgtc 300  
 tctgatgagc tgagaaacaa agccacccag ccaatgaagt ctgtactctg gtggcttcca 360  
 gtggaaaagg cattttggag gcagcctgca ggtcctggct ctggcatccg agagagactg 420  
 gagcaccagc tgttacacgt gagctggaat gacgcccgtg cctactgtgc ttggcgggga 480  
 aaacgactgc ccacggagga agagtgggag tttgccgccc gagggggctt gaaggggtcaa 540  
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 cccaagggag acaaagctga ggatggcttc catggagtct cccagtgaa tgctttcccc 660  
 gccagaaca actacgggct ctatgacctc ctggggaacg tgtgggagtg gacagcatca 720  
 ccgtaccagg ctgctgagca ggacatgcgc gtcctccggg gggcatcctg gatcgacaca 780  
 gctgatggct ctgccaatca ccgggcccgg gtcaccacca ggatgggcaa cactccagat 840  
 tcagcctcag acaacctcgg tttccgctgt gctgcagacg caggccggcc gccaggggag 900  
 ctgtaa 906

<210> 46  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 46

Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val  
 1 5 10 15

Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln  
 20 25 30

Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg  
 35 40 45

Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile  
50 55 60

Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu  
65 70 75 80

Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe  
85 90 95

Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met  
100 105 110

Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln  
115 120 125

Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val  
130 135 140

Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly  
145 150 155 160

Lys Arg Leu Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly  
165 170 175

Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg  
180 185 190

Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp  
195 200 205

Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn  
210 215 220

Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser  
225 230 235 240

Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser  
245 250 255

Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr  
260 265 270

Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe  
 275 280 285

Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu  
 290 295 300

<210> 47  
 <211> 927  
 <212> DNA  
 <213> Mus musculus

<400> 47  
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 ctgccaggtg gccggtttct gatggggaca gacgctccag atggcagaga cgggtgaagg 180  
 cctgccccgg aagtgcagct aaaacccttt gccatcgaca tatttccagt caccaataaa 240  
 gacttcaggg agtttgtcag ggagaagaag taccagactg aagccgaggc attcgggtgg 300  
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 gtgtgggagt ggacagcgtc cacatacaca cctgctggcc aggacatgcg tgcctccgg 780  
 ggggcatcat ggatcgacac cgcagacggc tctgctaata acagggctcg ggtcaccacc 840  
 aggatgggaa aactccaga ctcagcctca gacaacctgg gcttccgctg cgcctccagt 900  
 gcaggccgac cgaaggagga cctgtga 927

<210> 48  
 <211> 308  
 <212> PRT  
 <213> Mus musculus

<400> 48

Met Arg Ser Glu Phe Trp Phe Pro Ser Met Gly Ser Leu Leu Pro Pro  
 1 5 10 15

Val Leu Leu Leu Arg Leu Leu Ser Cys Pro Arg Leu Gln Leu Gly His  
 20 25 30

Ala Gln Asp Pro Ala Met Val His Leu Pro Gly Gly Arg Phe Leu Met  
 35 40 45

Gly Thr Asp Ala Pro Asp Gly Arg Asp Gly Glu Gly Pro Ala Arg Glu  
 50 55 60

Val Thr Val Lys Pro Phe Ala Ile Asp Ile Phe Pro Val Thr Asn Lys  
 65 70 75 80

Asp Phe Arg Glu Phe Val Arg Glu Lys Lys Tyr Gln Thr Glu Ala Glu  
 85 90 95

Ala Phe Gly Trp Ser Phe Val Phe Glu Asp Phe Val Ser Pro Glu Leu  
 100 105 110

Arg Lys Gln Glu Asn Leu Met Pro Ala Val His Trp Trp Gln Pro Val  
 115 120 125

Pro Lys Ala Phe Trp Arg Gln Pro Ala Gly Pro Gly Ser Gly Ile Arg  
 130 135 140

Glu Lys Leu Glu Leu Pro Val Val His Val Ser Trp Asn Asp Ala Gly  
 145 150 155 160

Ala Tyr Cys Ala Trp Arg Gly Arg Arg Leu Pro Thr Glu Glu Glu Trp  
 165 170 175

Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly Gln Val Tyr Pro Trp Gly  
 180 185 190

Asn Arg Phe Gln Pro Asn Arg Thr Asn Leu Trp Gln Gly Lys Phe Pro  
 195 200 205

Lys Gly Asp Lys Ala Glu Asp Gly Phe His Gly Leu Ser Pro Val Asn  
 210 215 220

Ala Phe Pro Pro Gln Asn Asn Tyr Gly Leu Tyr Asp Leu Met Gly Asn  
 225 230 235 240



Val Trp Glu Trp Thr Ala Ser Thr Tyr Gln Pro Ala Gly Gln Asp Met  
 245 250 255

Arg Val Leu Arg Gly Ala Ser Trp Ile Asp Thr Ala Asp Gly Ser Ala  
 260 265 270

Asn His Arg Ala Arg Val Thr Thr Arg Met Gly Asn Thr Pro Asp Ser  
 275 280 285

Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala Ser Ser Ala Gly Arg Pro  
 290 295 300

Lys Glu Asp Leu  
 305

<210> 49  
 <211> 855  
 <212> DNA  
 <213> Mus musculus

<400> 49  
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 gtcagcaatg cggattttga gaagtttgtg aactcgactg gctattttgac agaggctgag 180  
 aagtttggag actctttcgt ctttgaaggc atgttgagcg agcaagtga aacgcatatc 240  
 caccaggcag ttgcagctgc tccatggtgg ttgcctgtca agggagctaa ttggagacac 300  
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 tggaacgatg ctgttgcccta ctgcacatgg gcgggcaaga ggttgccctac tgaggcagag 420  
 tgggaataca gctgtagagg aggcctgcag aacaggcttt tcccctgggg caacaaactg 480  
 cagcccaaag gacagcatta tgccaacatc tggcagggca agtttcctgt gagcaacact 540  
 ggcgaggatg gcttccaagg aactgcccc gttgatgcct ttcctcccaa tggctatggc 600  
 ttatacaaca tagtggggaa tgtgtgggag tggacctcag actggtggac tgttcacat 660  
 tctgttgagg aaacgttcaa cccaaagggc cccacttctg ggaaagaccg agtgaagaag 720  
 ggtggatcct acatgtgcc taagtcctat tgctataggt accgctgtgc agctcgaagc 780  
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 cccaccgcag actga 855

<210> 50  
 <211> 284  
 <212> PRT  
 <213> Mus musculus

<400> 50

Met Val Pro Ile Pro Ala Gly Val Phe Thr Met Gly Thr Asp Asp Pro  
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Gln Ile Arg Gln Asp Gly Glu Ala Pro Ala Arg Arg Val Thr Val Asp  
 20 25 30

Gly Phe Tyr Met Asp Ala Tyr Glu Val Ser Asn Ala Asp Phe Glu Lys  
 35 40 45

Phe Val Asn Ser Thr Gly Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp  
 50 55 60

Ser Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr His Ile  
 65 70 75 80

His Gln Ala Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly Ala  
 85 90 95

Asn Trp Arg His Pro Glu Gly Pro Asp Ser Ser Ile Leu His Arg Ser  
 100 105 110

Asn His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr Cys  
 115 120 125

Thr Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser  
 130 135 140

Cys Arg Gly Gly Leu Gln Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu  
 145 150 155 160

Gln Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Lys Phe Pro  
 165 170 175

Val Ser Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val Asp  
 180 185 190

Ala Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn Val

195

200

205

Trp Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu Glu  
 210 215 220

Thr Phe Asn Pro Lys Gly Pro Thr Ser Gly Lys Asp Arg Val Lys Lys  
 225 230 235 240

Gly Gly Ser Tyr Met Cys His Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys  
 245 250 255

Ala Ala Arg Ser Gln Asn Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly  
 260 265 270

Phe Arg Cys Ala Ala Asp His Leu Pro Thr Ala Asp  
 275 280

&lt;210&gt; 51

&lt;211&gt; 1011

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;400&gt; 51

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gtgtgccagc aacgagcaca ggggtgcacac agccactacc gggattacta tggcgaactg      180
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tacatcgaca agtatgaggt ttccaacgaa gcctttgcga agtttgttct gcacactaac      360
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cggttgccca gcgaggcgga gtgggaggcg gcttgacagg gcggaagga gcgcaaactg      660
tttccttggg gcaacaagct gatgccaagg aatgaacatt ggctgaacat ctggcaggga      720
gactttcccg atggcaacct ggctgaagat gggtttgagt acaccagccc cgtggatgcc      780
ttccgacaga atatttacga cctgcacaac atggtgggca acgtctggga gtggacggca      840

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 gaagacagtt cagccggtaa cctggggtttt cgggtgcgcca agaatgcgtg a 1011

<210> 52  
 <211> 336  
 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 52

Met Thr Thr Ile Ile Leu Val Leu Phe Ile Trp Ile Val Leu Phe Asn  
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Asp Val Ser Ser Asp Cys Gly Cys Gln Lys Leu Asp Arg Lys Ala Pro  
 20 25 30

Asp Met Pro Ser Ile Ser Gly Gln Val Cys Gln Gln Arg Ala Gln Gly  
 35 40 45

Ala His Ser His Tyr Arg Asp Tyr Tyr Gly Glu Leu Glu Pro Asn Ile  
 50 55 60

Ala Asp Met Ser Leu Leu Pro Gly Gly Thr Val Tyr Met Gly Thr Asp  
 65 70 75 80

Lys Pro His Phe Pro Ala Asp Arg Glu Ala Pro Glu Arg Gln Val Lys  
 85 90 95

Leu Asn Asp Phe Tyr Ile Asp Lys Tyr Glu Val Ser Asn Glu Ala Phe  
 100 105 110

Ala Lys Phe Val Leu His Thr Asn Tyr Thr Thr Glu Ala Glu Arg Tyr  
 115 120 125

Gly Asp Ser Phe Leu Phe Lys Ser Leu Leu Ser Pro Leu Glu Gln Lys  
 130 135 140

Asn Leu Glu Asp Phe Arg Val Ala Ser Ala Val Trp Trp Tyr Lys Val  
 145 150 155 160

Ala Gly Val Asn Trp Arg His Pro Asn Gly Val Asp Ser Asp Ile Asp  
 165 170 175

His Leu Gly Arg His Pro Val Val His Val Ser Trp Arg Asp Ala Val  
 180 185 190

Glu Tyr Cys Lys Trp Ala Gly Lys Arg Leu Pro Ser Glu Ala Glu Trp  
 195 200 205

Glu Ala Ala Cys Arg Gly Gly Lys Glu Arg Lys Leu Phe Pro Trp Gly  
 210 215 220

Asn Lys Leu Met Pro Arg Asn Glu His Trp Leu Asn Ile Trp Gln Gly  
 225 230 235 240

Asp Phe Pro Asp Gly Asn Leu Ala Glu Asp Gly Phe Glu Tyr Thr Ser  
 245 250 255

Pro Val Asp Ala Phe Arg Gln Asn Ile Tyr Asp Leu His Asn Met Val  
 260 265 270

Gly Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Val Asn Asp Val  
 275 280 285

Ser Asp Asn Pro Asn Arg Val Lys Lys Gly Gly Ser Tyr Leu Cys His  
 290 295 300

Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn Thr  
 305 310 315 320

Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe Arg Cys Ala Lys Asn Ala  
 325 330 335

<210> 53  
 <211> 870  
 <212> DNA  
 <213> Anopheles gambiae

<400> 53  
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 ccggccccggc ccgcgacgat ccgcgacttt tacctcgacc agtacgaagt ctccaacgca 180  
 cagttcaagg cattcgtcga ccagacgggc tacgtcacgg aggcggaaaa gtttggcgac 240  
 agcttcgtct tccagcagct gtcagcgaa ccggtgcgcc agcagtacga agatttccgc 300

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gatgtgtcac gtgatataag cgaccgattg gaccatccgg tgggtgcacgt gtccctggaac 420
gatgcggtcg cgtactgcg cctggaaaggg aagcgccctgc cgacggaagc ggaatgggaa 480
gcggcctgcc ggggcggtcg caagcagaag ctgttcccct ggggtaacaa gctgatgccg 540
aaggagcagc acatgatgaa catatggcag ggcgagttcc cggacagcaa tctgaaggag 600
gatggctacg agaccacctg cccggtgacg tccttcgcc agaaccggtt cgagctgtac 660
aacatcggtg gcaacgtgtg ggagtggacg gcggatcttt gggacgcgaa ggatgcggcc 720
atcgagcgca agccgggcag cgatccaccg aatcgggtga aaaagggtgg ctcatacctg 780
tgtcacgaat cgtactgcta tcgctatcgc tgtgcggctc gatcgagaa caccgaggac 840
agttcggcgg gcaatctggg cttccggtgc 870

```

```

<210> 54
<211> 290
<212> PRT
<213> Anopheles gambiae

```

```

<400> 54

```

```

Pro Glu Ser Leu Leu Asp Leu Val Glu His Ser Lys Arg Phe Glu Asp
1           5           10          15

```

```

Met Ser Leu Ile Pro Gly Gly Glu Tyr Val Ile Gly Thr Asn Glu Pro
          20          25          30

```

```

Ile Phe Val Lys Asp Arg Glu Ser Pro Ala Arg Pro Ala Thr Ile Arg
          35          40          45

```

```

Asp Phe Tyr Leu Asp Gln Tyr Glu Val Ser Asn Ala Gln Phe Lys Ala
          50          55          60

```

```

Phe Val Asp Gln Thr Gly Tyr Val Thr Glu Ala Glu Lys Phe Gly Asp
65          70          75          80

```

```

Ser Phe Val Phe Gln Gln Leu Leu Ser Glu Pro Val Arg Gln Gln Tyr
          85          90          95

```

```

Glu Asp Phe Arg Val Ala Ala Ala Pro Trp Trp Tyr Lys Val Arg Gly
          100          105          110

```

```

Ala Ser Trp Gln His Pro Glu Gly Asp Val Ser Arg Asp Ile Ser Asp

```

115	120	125
Arg Leu Asp His Pro Val Val His Val Ser Trp Asn Asp Ala Val Ala		
130	135	140
Tyr Cys Ala Trp Lys Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu		
145	150	155 160
Ala Ala Cys Arg Gly Gly Arg Lys Gln Lys Leu Phe Pro Trp Gly Asn		
	165 170	175
Lys Leu Met Pro Lys Glu Gln His Met Met Asn Ile Trp Gln Gly Glu		
	180 185	190
Phe Pro Asp Ser Asn Leu Lys Glu Asp Gly Tyr Glu Thr Thr Cys Pro		
	195 200	205
Val Thr Ser Phe Arg Gln Asn Pro Phe Glu Leu Tyr Asn Ile Val Gly		
	210 215	220
Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Ala Lys Asp Ala Ala		
225	230 235	240
Ile Glu Arg Lys Pro Gly Ser Asp Pro Pro Asn Arg Val Lys Lys Gly		
	245 250	255
Gly Ser Tyr Leu Cys His Glu Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala		
	260 265	270
Ala Arg Ser Gln Asn Thr Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe		
	275 280	285
Arg Cys		
290		

&lt;210&gt; 55

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Streptomyces coelicolor

&lt;400&gt; 55

gtggccgtgg ccgccccgtc ccccgcggcc gccgcggagc cggggcccgcc cgcccgctccg 60

cgctcgaccc gcggacaggt gcgcctgccg ggcggtgagt tcgcgatggg ggacgccttc 120

```

ggggagggat atccggccga cggcgagaca cccgtgcaca cggtgcgctt gcggcccttc 180
cacatcgacg agaccgccgt caccaacgcc cggttcgccg ccttcgtcaa ggcgaccggc 240
catgtgaccg acgccgaacg cttcggctcc tcggccgtct tccacctggt cgtcgccgcc 300
ccggacgccg acgtcctcgg cagcgccgcc ggcgccccct ggtggatcaa cgtgcggggc 360
gcccactggc gccgccccga gggcgcccg cccgacatca ccggccggcc gaaccatccg 420
gtcgtccacg tctcctggaa cgatgccacc gcctacgcgc ggtgggcccg caagcgctg 480
cccaccgagg ccgaatggga gtacgccgc cgcgggggac tggccggccg ccgctacgcc 540
tggggcgacg agctgacccc gggcgggccg tggcgctgca acatctggca gggccgcttc 600
ccgcacgtca acacggccga ggacgggcac ctgagcaccg caccggtcaa gtcctaccgg 660
cccaacggcc acggcctgtg gaacaccgcg ggcaacgtgt gggaatggtg ctccgactgg 720
ttctcgccca cctactacgc cgaatcacc accgtcgacc cgcacggccc cgggaccggg 780
gcggcacggg tgctgcgcgg cggctcctac ctgtgccacg actcctactg caaccgctac 840
cgggtcgccg cccgctcctc caacaccccg gactcctcgt ccggcaacct cggattccgc 900
tgcgccaacg acgcgacact cacgtccgga tcagccgctg agtga 945

```

```

<210> 56
<211> 314
<212> PRT
<213> Streptomyces coelicolor

```

```
<400> 56
```

```

Met Ala Val Ala Ala Pro Ser Pro Ala Ala Ala Ala Glu Pro Gly Pro
1           5           10          15

```

```

Ala Ala Arg Pro Arg Ser Thr Arg Gly Gln Val Arg Leu Pro Gly Gly
          20          25          30

```

```

Glu Phe Ala Met Gly Asp Ala Phe Gly Glu Gly Tyr Pro Ala Asp Gly
          35          40          45

```

```

Glu Thr Pro Val His Thr Val Arg Leu Arg Pro Phe His Ile Asp Glu
          50          55          60

```

```

Thr Ala Val Thr Asn Ala Arg Phe Ala Ala Phe Val Lys Ala Thr Gly
65          70          75          80

```

```

His Val Thr Asp Ala Glu Arg Phe Gly Ser Ser Ala Val Phe His Leu

```



85

90

95

Val Val Ala Ala Pro Asp Ala Asp Val Leu Gly Ser Ala Ala Gly Ala  
 100 105 110

Pro Trp Trp Ile Asn Val Arg Gly Ala His Trp Arg Arg Pro Glu Gly  
 115 120 125

Ala Arg Ser Asp Ile Thr Gly Arg Pro Asn His Pro Val Val His Val  
 130 135 140

Ser Trp Asn Asp Ala Thr Ala Tyr Ala Arg Trp Ala Gly Lys Arg Leu  
 145 150 155 160

Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Leu Ala Gly  
 165 170 175

Arg Arg Tyr Ala Trp Gly Asp Glu Leu Thr Pro Gly Gly Arg Trp Arg  
 180 185 190

Cys Asn Ile Trp Gln Gly Arg Phe Pro His Val Asn Thr Ala Glu Asp  
 195 200 205

Gly His Leu Ser Thr Ala Pro Val Lys Ser Tyr Arg Pro Asn Gly His  
 210 215 220

Gly Leu Trp Asn Thr Ala Gly Asn Val Trp Glu Trp Cys Ser Asp Trp  
 225 230 235 240

Phe Ser Pro Thr Tyr Tyr Ala Glu Ser Pro Thr Val Asp Pro His Gly  
 245 250 255

Pro Gly Thr Gly Ala Ala Arg Val Leu Arg Gly Gly Ser Tyr Leu Cys  
 260 265 270

His Asp Ser Tyr Cys Asn Arg Tyr Arg Val Ala Ala Arg Ser Ser Asn  
 275 280 285

Thr Pro Asp Ser Ser Ser Gly Asn Leu Gly Phe Arg Cys Ala Asn Asp  
 290 295 300

Ala Asp Leu Thr Ser Gly Ser Ala Ala Glu  
 305 310

<210> 57  
 <211> 1005  
 <212> DNA  
 <213> *Corynebacterium efficiens*

<400> 57  
 gtgggttcgcc atcgactggg ccaccggccc tgcacactga ggattacgtc catgagtaac 60  
 tgctgctccc cgtcaagcgc acaatggcgt accactaccc gggatttata agatcctgtc 120  
 aatcccacca ctccatgcaa cccggaacaa tcccgcgatg ctgtgacact gccgggtgga 180  
 gctttccaca tgggcgatca tcacggggag gggatcccg cggacgggga ggggccagta 240  
 catgaggttc acctcgcccc cttcggcatt aatgtcacca cggtcacgaa tgccgagttc 300  
 ggacgattta ttgaagccac aggggtatacg acgacagcgg aacgctacgg tgtctcggct 360  
 gtattctacg cagcgttcca agggcaacgc gctgacattc ttcgccaggt tcccggcgtg 420  
 ccctggtggc tggcgggtcaa ggggtgcgaac tggcagcgtc ccaacggccc cggatccacc 480  
 ctggacgggc ttgaggacca ccccgtcggt cacgtttcct gggatgatgc cgttgccctac 540  
 tgcacctggg ctggcgggtcg tctgcccacc gaagccgagt ggggaatacgc cggccggggt 600  
 ggactgcagg gcgcacgata tgcctggggg gataacctcg ccctagacgg gaggtggaac 660  
 tgcaatatct ggcagggggg cttcccatg gagaacaccg ccgcggatgg ttacctcacc 720  
 actgcaccgg tgaagacctc cacgcccatt ggatacggtc tgtggcagat ggcagggaat 780  
 gtatgggaat ggtgccagga ctggtttgat gcggagtact actcccgtgc ttctccatc 840  
 aaccgcggg gaccggatac cgggtgcgcgc cgggtgatgc gcggaggctc gtatctctgc 900  
 catgattcct actgcaacag ataccgggtg gccgcccgc attcgaacac cccggattcc 960  
 acctcgggga ataccggttt ccggtgcggt ttcgatagtc cttga 1005

<210> 58  
 <211> 334  
 <212> PRT  
 <213> *Corynebacterium efficiens*

<400> 58

Met Val Arg His Arg Leu Gly His Arg Pro Cys Thr Leu Arg Ile Thr  
 1 5 10 15

Ser Met Ser Asn Cys Cys Ser Pro Ser Ser Ala Gln Trp Arg Thr Thr  
 20 25 30

Thr Arg Asp Leu Ser Asp Pro Val Asn Pro Thr Thr Pro Cys Asn Pro  
 35 40 45

Glu Gln Ser Arg Asp Ala Val Thr Leu Pro Gly Gly Ala Phe His Met  
 50 55 60

Gly Asp His His Gly Glu Gly Tyr Pro Ala Asp Gly Glu Gly Pro Val  
 65 70 75 80

His Glu Val His Leu Ala Pro Phe Gly Ile Asn Val Thr Thr Val Thr  
 85 90 95

Asn Ala Glu Phe Gly Arg Phe Ile Glu Ala Thr Gly Tyr Thr Thr Thr  
 100 105 110

Ala Glu Arg Tyr Gly Val Ser Ala Val Phe Tyr Ala Ala Phe Gln Gly  
 115 120 125

Gln Arg Ala Asp Ile Leu Arg Gln Val Pro Gly Val Pro Trp Trp Leu  
 130 135 140

Ala Val Lys Gly Ala Asn Trp Gln Arg Pro Asn Gly Pro Gly Ser Thr  
 145 150 155 160

Leu Asp Gly Leu Glu Asp His Pro Val Val His Val Ser Trp Asp Asp  
 165 170 175

Ala Val Ala Tyr Cys Thr Trp Ala Gly Gly Arg Leu Pro Thr Glu Ala  
 180 185 190

Glu Trp Glu Tyr Ala Ala Arg Gly Gly Leu Gln Gly Ala Arg Tyr Ala  
 195 200 205

Trp Gly Asp Asn Leu Ala Leu Asp Gly Arg Trp Asn Cys Asn Ile Trp  
 210 215 220

Gln Gly Gly Phe Pro Met Glu Asn Thr Ala Ala Asp Gly Tyr Leu Thr  
 225 230 235 240

Thr Ala Pro Val Lys Thr Tyr Thr Pro Asn Gly Tyr Gly Leu Trp Gln  
 245 250 255

Met Ala Gly Asn Val Trp Glu Trp Cys Gln Asp Trp Phe Asp Ala Glu  
 260 265 270

Tyr Tyr Ser Arg Ala Ser Ser Ile Asn Pro Arg Gly Pro Asp Thr Gly  
 275 280 285

Ala Arg Arg Val Met Arg Gly Gly Ser Tyr Leu Cys His Asp Ser Tyr  
 290 295 300

Cys Asn Arg Tyr Arg Val Ala Ala Arg Asn Ser Asn Thr Pro Asp Ser  
 305 310 315 320

Thr Ser Gly Asn Thr Gly Phe Arg Cys Val Phe Asp Ser Pro  
 325 330

<210> 59

<211> 1017

<212> DNA

<213> Novosphingobium aromaticivorans

<400> 59

atggcgcaac cattccgatac gacggcgggcc agtcgtacaa gtattgaacg ccatctcgaa	60
cccaattgca ggagcacgtc gcgaatggtc gaacgccccg gcatgcgcct gatcgaaggc	120
ggcactttca ccatgggctc ggaagccttc taccgaggagg aagcgccgct tcgccgggtg	180
aaggtagaca gcttctggat cgatgaagcg ccggtgacga acgcacagtt cgccgcatte	240
gtggaggcca cgggatacgt cactgtggcc gagatcgagc cggatcccaa ggactacccc	300
ggcatgctcc cgggcatgga ccgcgcggga tcgctgggtgt tccagaaaac agcagggccg	360
gtcgacatgg cggatgcgtc caactggtgg cactttacct ttggcgccctg ctggaagcat	420
ccacttgga cgggcagttc catcgatggg atcgaggacc atcccgtcgt tcacgtcgcc	480
tatgccgatg ccgaggccta tgccaaatgg gcgggcaagg atctgccgac cgaagccgag	540
ttcgaatatg ctgcgcgcgg cgggttgga ggttcggaat tttcctgggg agacgaactc	600
gcacctgaag gccggatgat ggccaactac tggcaaggcc tgtttccctt cgccaaccag	660
tgccctgatg gctgggaacg gacatcgccc gtccgcaact tcccgcccaa cggctatggt	720
ctttacgaca tgatcgggaa cacgtgggag tggacctgcg attggtgggc cgacaagccg	780
ctgactccgc aaaggaaatc ggcattgctgc gcgatcagca atccgcgcgg cggcaagctc	840
aaggacagct tcgaccgctc gcaaccgcga atgcgcacgc gccggaaggc cataaagggc	900
ggttcgcacc tgtgtgcggc caattactgc cagcgtatc gccccgcagc acgcatcct	960

gaaatggttg ataccgcgac gacgcacatc ggcttcaggt gtgtggtgcg gccctga 1017

<210> 60  
 <211> 338  
 <212> PRT  
 <213> Novosphingobium aromaticivorans

<400> 60

Met Ala Gln Pro Phe Arg Ser Thr Ala Ala Ser Arg Thr Ser Ile Glu  
 1 5 10 15

Arg His Leu Glu Pro Asn Cys Arg Ser Thr Ser Arg Met Val Glu Arg  
 20 25 30

Pro Gly Met Arg Leu Ile Glu Gly Gly Thr Phe Thr Met Gly Ser Glu  
 35 40 45

Ala Phe Tyr Pro Glu Glu Ala Pro Leu Arg Arg Val Lys Val Asp Ser  
 50 55 60

Phe Trp Ile Asp Glu Ala Pro Val Thr Asn Ala Gln Phe Ala Ala Phe  
 65 70 75 80

Val Glu Ala Thr Gly Tyr Val Thr Val Ala Glu Ile Glu Pro Asp Pro  
 85 90 95

Lys Asp Tyr Pro Gly Met Leu Pro Gly Met Asp Arg Ala Gly Ser Leu  
 100 105 110

Val Phe Gln Lys Thr Ala Gly Pro Val Asp Met Ala Asp Ala Ser Asn  
 115 120 125

Trp Trp His Phe Thr Phe Gly Ala Cys Trp Lys His Pro Leu Gly Pro  
 130 135 140

Gly Ser Ser Ile Asp Gly Ile Glu Asp His Pro Val Val His Val Ala  
 145 150 155 160

Tyr Ala Asp Ala Glu Ala Tyr Ala Lys Trp Ala Gly Lys Asp Leu Pro  
 165 170 175

Thr Glu Ala Glu Phe Glu Tyr Ala Ala Arg Gly Gly Leu Asp Gly Ser  
 180 185 190

Glu Phe Ser Trp Gly Asp Glu Leu Ala Pro Glu Gly Arg Met Met Ala  
 195 200 205

Asn Tyr Trp Gln Gly Leu Phe Pro Phe Ala Asn Gln Cys Leu Asp Gly  
 210 215 220

Trp Glu Arg Thr Ser Pro Val Arg Asn Phe Pro Pro Asn Gly Tyr Gly  
 225 230 235 240

Leu Tyr Asp Met Ile Gly Asn Thr Trp Glu Trp Thr Cys Asp Trp Trp  
 245 250 255

Ala Asp Lys Pro Leu Thr Pro Gln Arg Lys Ser Ala Cys Cys Ala Ile  
 260 265 270

Ser Asn Pro Arg Gly Gly Lys Leu Lys Asp Ser Phe Asp Pro Ser Gln  
 275 280 285

Pro Ala Met Arg Ile Gly Arg Lys Val Ile Lys Gly Gly Ser His Leu  
 290 295 300

Cys Ala Ala Asn Tyr Cys Gln Arg Tyr Arg Pro Ala Ala Arg His Pro  
 305 310 315 320

Glu Met Val Asp Thr Ala Thr Thr His Ile Gly Phe Arg Cys Val Val  
 325 330 335

Arg Pro

<210> 61  
 <211> 1119  
 <212> DNA  
 <213> Mesorhizobium loti

<400> 61  
 atgggccac gaggtcgagg tcaaaaaccg catgaaaggc gacgcggtca tgttcgacat 60  
 tgccgggaag ttctagccga tagcgggtgg gcggtgatg gagatgagca cgccgtgtca 120  
 tttcgggatc tttcgatgaa cgcccctgcc gaagtcttcg agcgcgctgc agccgaacgg 180  
 tcgtaccccg gaatggtctg gatccccggc ggtaccttcc tgatgggctc agacaaccac 240  
 tatccggagg aggcaccggc ccaccgggtc agggtcgacg gcttctggat ggacaaattc 300

```

accgtctcca accgcgactt cgaacgcttc gttgcggcga caggacatgt cactcttgcc 360
gagaaacccg ccaatcccga cgactatccc ggtgccttac ccgatctgct ggctccgtcc 420
tcgatgatgt tcaggaagcc ggccggccct gtcgaccttg gcaatcacta caattggtgg 480
gtctatgtcc gcggcgccaa ctggcgccat ccacgcgggc cggcaagtac aatcaagaag 540
gttgagatc atccggtcgt gcatgtggcc tacgaggatg tcgtggccta tgccaactgg 600
gcaggcaagg aacttcccac cgaggccgag tgggaattcg cggcgcgagg cggcctcgat 660
gccgccgaat acgtctgggg caacgagctt acgccggccg ggaagcacat ggccaacatc 720
tggcaaggag actttcccta ccggaatact gtcgacgacg gttacgaata tacggcccca 780
gtaggctcgt tcccggccaa cgactacggt ctctacgaca tggccggcaa tgtctggcaa 840
tggaagaccg actggtacca ggaccacaag gcgatcgaca gcccgctgctg caccgctgtc 900
aatccgctg gcggccatcg cgaagcgagc tatgacaccc ggctacctga cgttaagatc 960
cctcgcaagg tcaccaaggg tggctcccat ctgtgcgcgc cgaactactg tcggcgctac 1020
cggcccgcgg cgcaatggc gcaaccgctc gacactgcaa tctcccatct cggctttcgc 1080
tgcacgtgc gaaggaaaat ggaattgaac gcgcagtaa 1119

```

<210> 62

<211> 372

<212> PRT

<213> Mesorhizobium loti

<400> 62

```

Met Gly Pro Arg Gly Arg Gly Gln Lys Pro His Glu Arg Arg Arg Gly
1           5           10          15

```

```

His Val Arg His Cys Arg Glu Val Leu Ala Asp Ser Gly Trp Ala Ala
          20          25          30

```

```

Asp Gly Asp Glu His Ala Val Ser Phe Arg Asp Leu Ser Met Asn Ala
          35          40          45

```

```

Pro Ala Glu Val Phe Glu Arg Ala Ala Ala Glu Arg Ser Tyr Pro Gly
          50          55          60

```

```

Met Val Trp Ile Pro Gly Gly Thr Phe Leu Met Gly Ser Asp Asn His
65          70          75          80

```

Tyr Pro Glu Glu Ala Pro Ala His Arg Val Arg Val Asp Gly Phe Trp  
                             85                            90                            95

Met Asp Lys Phe Thr Val Ser Asn Arg Asp Phe Glu Arg Phe Val Ala  
                             100                            105                            110

Ala Thr Gly His Val Thr Leu Ala Glu Lys Pro Ala Asn Pro Asp Asp  
                             115                            120                            125

Tyr Pro Gly Ala Leu Pro Asp Leu Leu Ala Pro Ser Ser Met Met Phe  
                             130                            135                            140

Arg Lys Pro Ala Gly Pro Val Asp Leu Gly Asn His Tyr Asn Trp Trp  
                             145                            150                            155                            160

Val Tyr Val Arg Gly Ala Asn Trp Arg His Pro Arg Gly Pro Ala Ser  
                             165                            170                            175

Thr Ile Lys Lys Val Ala Asp His Pro Val Val His Val Ala Tyr Glu  
                             180                            185                            190

Asp Val Val Ala Tyr Ala Asn Trp Ala Gly Lys Glu Leu Pro Thr Glu  
                             195                            200                            205

Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Asp Ala Ala Glu Tyr  
                             210                            215                            220

Val Trp Gly Asn Glu Leu Thr Pro Ala Gly Lys His Met Ala Asn Ile  
                             225                            230                            235                            240

Trp Gln Gly Asp Phe Pro Tyr Arg Asn Thr Val Asp Asp Gly Tyr Glu  
                             245                            250                            255

Tyr Thr Ala Pro Val Gly Ser Phe Pro Ala Asn Asp Tyr Gly Leu Tyr  
                             260                            265                            270

Asp Met Ala Gly Asn Val Trp Gln Trp Thr Thr Asp Trp Tyr Gln Asp  
                             275                            280                            285

His Lys Ala Ile Asp Ser Pro Cys Cys Thr Ala Val Asn Pro Arg Gly  
                             290                            295                            300

Gly His Arg Glu Ala Ser Tyr Asp Thr Arg Leu Pro Asp Val Lys Ile



305                      310                      315                      320  
 Pro Arg Lys Val Thr Lys Gly Gly Ser His Leu Cys Ala Pro Asn Tyr  
                                  325                                   330                                   335  
 Cys Arg Arg Tyr Arg Pro Ala Ala Arg Met Ala Gln Pro Val Asp Thr  
                                  340                                   345                                   350  
 Ala Ile Ser His Leu Gly Phe Arg Cys Ile Val Arg Arg Lys Met Glu  
                                  355                                   360                                   365  
 Leu Asn Ala Gln  
                                  370

<210> 63  
 <211> 1251  
 <212> DNA  
 <213> Burkholderia fungorum

<400> 63  
 atgaagagtg aaagagatcg agagcccgca aagtcgtccc gctcgaacgg gtcggtcgca 60  
 gcaacccaaa cgcgcgccgg tcgctgctgc aaactaatgt tgtggggcgc cctgctcgtc 120  
 atactgcccc cctgtgtcgg cgccgcggtc agttgggcct tcacgccgca cgcacccgct 180  
 caccgcgaaa tcgttttcgg cgacggcacg catggtccgc tcggcatggc gtgggtgccc 240  
 ggcgggccagt tcctcatggg cagcgacgcc aaacaggcgc aaccgaacga acgccccgcg 300  
 cacaaggtca aggtgcacgg cttctggatg gaccgccatc acgtgaccaa cgccgaattc 360  
 cgccgcttcg tcgaagcgac cggctacgtc accacggccg agaagaaacc cgactgggag 420  
 accctgaaag tccagttgcc gcccggcacg ccgcgcccgc ccgagagcgc gatggtggcg 480  
 ggtgcaatgg tgttcgtcgg caccagccgt cccgtgccgc tagacgacta ttcgcagtgg 540  
 tggcgctatg tgcctggcgc taactggcgt catccagccg ggctgagag caacatcatc 600  
 ggtaaagatg atcaccccggt ggttcaagtg tcctacgaag atgcgcaggc ttatgcgaaa 660  
 tgggcccggca agcgtctgcc gaccgaagcc gaatgggaat tcgccgcgcg cggcggcctc 720  
 gaacaggcca cgtatgcgtg gggcgatcag ttctctccca acggcaaaca gatggccaac 780  
 gtctggcagg gccagcagcc gcagtcttcc cccgttgtca acccgaaagc ggggtggcgcg 840  
 ctcggtacaa gtccggtggg tactttcccg gccaacggct acggccttcc cgacatgacc 900  
 ggcaacgcct ggcagtgggt tgccgactgg tatcgcgcgg atcagttcag gcgtgaggcg 960

gtaagcacca ggcgcgatcga caatccggtg ggcccagagcg agtcgtggga ccccgagac 1020  
cagggcgtgc ccgtcaacgc gcccaagcgt gtcacacgcg gcggttcgtt cctctgcaac 1080  
gaaatctatt gcctgagcta ccggcccagc gcgagacgcg gcaccgatcc ctacaacagc 1140  
atgtcgcatac tgggcttccg gctggtgatg gacgaagaca cctggaaaga agccggtgct 1200  
cgccaggctt cggcgaaagc tgccggcgcg cctggaaccc ctggcggcta g 1251

<210> 64

<211> 416

<212> PRT

<213> Burkholderia fungorum

<400> 64

Met Lys Ser Glu Arg Asp Arg Glu Pro Ala Lys Ser Ser Arg Ser Asn  
1 5 10 15

Gly Ser Val Ala Ala Thr Gln Thr Arg Ala Gly Arg Val Arg Lys Leu  
20 25 30

Met Leu Trp Gly Ala Leu Leu Val Ile Leu Pro Ala Cys Val Gly Ala  
35 40 45

Ala Val Ser Trp Ala Phe Thr Pro His Ala Pro Ala His Pro Gln Ile  
50 55 60

Val Phe Gly Asp Gly Thr His Gly Pro Leu Gly Met Ala Trp Val Pro  
65 70 75 80

Gly Gly Gln Phe Leu Met Gly Ser Asp Ala Lys Gln Ala Gln Pro Asn  
85 90 95

Glu Arg Pro Ala His Lys Val Lys Val His Gly Phe Trp Met Asp Arg  
100 105 110

His His Val Thr Asn Ala Glu Phe Arg Arg Phe Val Glu Ala Thr Gly  
115 120 125

Tyr Val Thr Thr Ala Glu Lys Lys Pro Asp Trp Glu Thr Leu Lys Val  
130 135 140

Gln Leu Pro Pro Gly Thr Pro Arg Pro Pro Glu Ser Ala Met Val Ala  
145 150 155 160

Gly Ala Met Val Phe Val Gly Thr Ser Arg Pro Val Pro Leu Asp Asp  
 165 170 175

Tyr Ser Gln Trp Trp Arg Tyr Val Pro Gly Ala Asn Trp Arg His Pro  
 180 185 190

Ala Gly Pro Glu Ser Asn Ile Ile Gly Lys Asp Asp His Pro Val Val  
 195 200 205

Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp Ala Gly Lys  
 210 215 220

Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu  
 225 230 235 240

Glu Gln Ala Thr Tyr Ala Trp Gly Asp Gln Phe Ser Pro Asn Gly Lys  
 245 250 255

Gln Met Ala Asn Val Trp Gln Gly Gln Gln Pro Gln Ser Phe Pro Val  
 260 265 270

Val Asn Pro Lys Ala Gly Gly Ala Leu Gly Thr Ser Pro Val Gly Thr  
 275 280 285

Phe Pro Ala Asn Gly Tyr Gly Leu Ser Asp Met Thr Gly Asn Ala Trp  
 290 295 300

Gln Trp Val Ala Asp Trp Tyr Arg Ala Asp Gln Phe Arg Arg Glu Ala  
 305 310 315 320

Val Ser Thr Ser Ala Ile Asp Asn Pro Val Gly Pro Ser Glu Ser Trp  
 325 330 335

Asp Pro Ala Asp Gln Gly Val Pro Val Asn Ala Pro Lys Arg Val Thr  
 340 345 350

Arg Gly Gly Ser Phe Leu Cys Asn Glu Ile Tyr Cys Leu Ser Tyr Arg  
 355 360 365

Pro Ser Ala Arg Arg Gly Thr Asp Pro Tyr Asn Ser Met Ser His Leu  
 370 375 380

Gly Phe Arg Leu Val Met Asp Glu Asp Thr Trp Lys Glu Ala Gly Ala  
 385 390 395 400

Arg Gln Ala Ser Ala Lys Ala Ala Gly Ala Pro Gly Thr Pro Gly Gly  
 405 410 415

<210> 65  
 <211> 912  
 <212> DNA  
 <213> *Sinorhizobium meliloti*

<400> 65  
 atggtctggg ttcccggagc gaccttcatg atggggtcga acgaccatta cccggaggaa 60  
 gcgcccgtgc atccggtaac cgtcgacgga ttctggatcg atgtgacacc ggtaacgaac 120  
 cgccagtttc tcgaattcgt aaatgcgacg gggcatgtga ccttcgcgga aagaaagccg 180  
 cgcgccgaag actatccggg cgctccgcca tccaatctaa gggccggttc gctcgtcttc 240  
 acacccccga agcgaccgct gcagggaacg gatatatcgc agtggtgatg attcacgctg 300  
 ggtgccaact ggcggcaccc gctcgggctc aagagcagca tcggagcgat tctggatcat 360  
 ccggtcgtcc atgtcgctta cagcgacgca aaggcctatg ccgaatgggc cggcaaggac 420  
 ctcccgaccg agaccgagtg ggagctggcg gcccgcggcg gcctcgatgg ggctgaattt 480  
 tcctggggcg gcgagcttgc gccgggcgga aatcacatgg ccaatacttg gcagggaggt 540  
 tttccggctc agaattctat ggacgatggt ttcgcgcgaa catcgccggt cagattttac 600  
 ccgccaacg gctacggcct ctacgacatg atcggaatg tgtgggagtg gaccacggat 660  
 tactggtccg tgcgccaccc ggaagcggcc gccaaagcctt gctgcattcc gagcaatccc 720  
 cgcaatgccg atgccgatgc gagtatcgat ccggcggcga gcgtgaaagt tccgcgccgg 780  
 gtgctcaagg gtggatcgca tctctgcgcg ccgaactact gccggcggtg ccgccctgcg 840  
 gcgaggcacg cccaggaaat cgacacgacg accagccatg tcggtttccg atgtgtcagg 900  
 cgcgttcgat aa 912

<210> 66  
 <211> 303  
 <212> PRT  
 <213> *Sinorhizobium meliloti*

<400> 66

Met Val Trp Val Pro Gly Ala Thr Phe Met Met Gly Ser Asn Asp His  
 1 5 10 15

Tyr Pro Glu Glu Ala Pro Val His Pro Val Thr Val Asp Gly Phe Trp  
 20 25 30

Ile Asp Val Thr Pro Val Thr Asn Arg Gln Phe Leu Glu Phe Val Asn  
 35 40 45

Ala Thr Gly His Val Thr Phe Ala Glu Arg Lys Pro Arg Ala Glu Asp  
 50 55 60

Tyr Pro Gly Ala Pro Pro Ser Asn Leu Arg Ala Gly Ser Leu Val Phe  
 65 70 75 80

Thr Pro Pro Lys Arg Pro Leu Gln Gly Thr Asp Ile Ser Gln Trp Trp  
 85 90 95

Ile Phe Thr Leu Gly Ala Asn Trp Arg His Pro Leu Gly Arg Lys Ser  
 100 105 110

Ser Ile Gly Ala Ile Leu Asp His Pro Val Val His Val Ala Tyr Ser  
 115 120 125

Asp Ala Lys Ala Tyr Ala Glu Trp Ala Gly Lys Asp Leu Pro Thr Glu  
 130 135 140

Thr Glu Trp Glu Leu Ala Ala Arg Gly Gly Leu Asp Gly Ala Glu Phe  
 145 150 155 160

Ser Trp Gly Gly Glu Leu Ala Pro Gly Gly Asn His Met Ala Asn Thr  
 165 170 175

Trp Gln Gly Ser Phe Pro Val Glu Asn Ser Met Asp Asp Gly Phe Ala  
 180 185 190

Arg Thr Ser Pro Val Arg Phe Tyr Pro Pro Asn Gly Tyr Gly Leu Tyr  
 195 200 205

Asp Met Ile Gly Asn Val Trp Glu Trp Thr Thr Asp Tyr Trp Ser Val  
 210 215 220

Arg His Pro Glu Ala Ala Ala Lys Pro Cys Cys Ile Pro Ser Asn Pro  
 225 230 235 240

Arg Asn Ala Asp Ala Asp Ala Ser Ile Asp Pro Ala Ala Ser Val Lys  
                   245                                  250                                  255

Val Pro Arg Arg Val Leu Lys Gly Gly Ser His Leu Cys Ala Pro Asn  
                   260                                  265                                  270

Tyr Cys Arg Arg Tyr Arg Pro Ala Ala Arg His Ala Gln Glu Ile Asp  
                   275                                  280                                  285

Thr Thr Thr Ser His Val Gly Phe Arg Cys Val Arg Arg Val Arg  
                   290                                  295                                  300

<210> 67  
 <211> 1065  
 <212> DNA  
 <213> Microscilla sp.

<400> 67  
 atgaaataca ttttttttagt tcttttctta tgggccttga cccgatgtac cggaaagtat 60  
 gaggacaaga gagtggaaac tgatacttcc agacaaaaag ccgaagcgtc agatataaaa 120  
 gttcccgaag gaatggctta tattcccgcg ggccagtaca tgatgggagg taaatcagac 180  
 caggcttata aggatgaata tccccgccat aacgtgaagg ttccggcttt ttatatggac 240  
 cttacagaag tgaccaatgc ggagtttaag cggtttgtag acgaaacggg ctacgtgacc 300  
 attgctgaga aagatattga ctgggaagag ttaaagtctc aggtgccaca gggtagccccg 360  
 aagcctcctg attctgtgct tcaggcaggt tcaactggttt tcaagcagac agatgaaccc 420  
 gtttctctcc aggattattc acagtgggtg gaatggacta tcggagccaa ctggcgaaat 480  
 ccggaggggtc caggtagtac gattgaggat cgtatggatc atccgggtgg acacgtttcc 540  
 tttgaagatg tccaagcgta tgcggattgg gccggtaagc gcctgcctac tgaggcagaa 600  
 tgggaatggg ccgccatggg aggccaaaat gacgtgaaat atccatgggg aaatgaatcg 660  
 gtogaacaag catccgataa agcaaacttt tggcagggga attttccaca tcaaaactat 720  
 gccctcgatg gattcgaacg caccgcccct gtacgctcct tcccagcgaa tgggtacggc 780  
 ctatatgata tggctggcaa tgtgtgggaa tgggtgccagg ataagtatga tgtcaatgct 840  
 tatgaaagct ataagcaaaa aggactgaca gaagacccca cgggttctga gcactacaac 900  
 gaccctaggg aaccgtatac tcctaagcat gtgatcagag ggggttcttt cctatgcaat 960  
 gacagctact gtagtgggta tcgtgtttca cgtcgtatga gttccagtag agattcaggt 1020  
 tttaatcata cgggattcag gtgtgtgaaa gatgtaaatt gatag 1065

<210> 68  
 <211> 354  
 <212> PRT  
 <213> Microscilla sp.

<400> 68

Met Lys Tyr Ile Phe Leu Val Leu Phe Leu Trp Ala Leu Thr Arg Cys  
 1 5 10 15

Thr Gly Lys Tyr Glu Asp Lys Arg Val Glu Thr Asp Thr Ser Arg Pro  
 20 25 30

Lys Ala Glu Ala Ser Asp Ile Lys Val Pro Glu Gly Met Ala Tyr Ile  
 35 40 45

Pro Ala Gly Gln Tyr Met Met Gly Gly Lys Ser Asp Gln Ala Tyr Lys  
 50 55 60

Asp Glu Tyr Pro Arg His Asn Val Lys Val Ser Ala Phe Tyr Met Asp  
 65 70 75 80

Leu Thr Glu Val Thr Asn Ala Glu Phe Lys Arg Phe Val Asp Glu Thr  
 85 90 95

Gly Tyr Val Thr Ile Ala Glu Lys Asp Ile Asp Trp Glu Glu Leu Lys  
 100 105 110

Ser Gln Val Pro Gln Gly Thr Pro Lys Pro Pro Asp Ser Val Leu Gln  
 115 120 125

Ala Gly Ser Leu Val Phe Lys Gln Thr Asp Glu Pro Val Ser Leu Gln  
 130 135 140

Asp Tyr Ser Gln Trp Trp Glu Trp Thr Ile Gly Ala Asn Trp Arg Asn  
 145 150 155 160

Pro Glu Gly Pro Gly Ser Thr Ile Glu Asp Arg Met Asp His Pro Val  
 165 170 175

Val His Val Ser Phe Glu Asp Val Gln Ala Tyr Ala Asp Trp Ala Gly  
 180 185 190

Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Trp Ala Ala Met Gly Gly  
 195 200 205

Gln Asn Asp Val Lys Tyr Pro Trp Gly Asn Glu Ser Val Glu Gln Ala  
 210 215 220

Ser Asp Lys Ala Asn Phe Trp Gln Gly Asn Phe Pro His Gln Asn Tyr  
 225 230 235 240

Ala Leu Asp Gly Phe Glu Arg Thr Ala Pro Val Arg Ser Phe Pro Ala  
 245 250 255

Asn Gly Tyr Gly Leu Tyr Asp Met Ala Gly Asn Val Trp Glu Trp Cys  
 260 265 270

Gln Asp Lys Tyr Asp Val Asn Ala Tyr Glu Ser Tyr Lys Gln Lys Gly  
 275 280 285

Leu Thr Glu Asp Pro Thr Gly Ser Glu His Tyr Asn Asp Pro Arg Glu  
 290 295 300

Pro Tyr Thr Pro Lys His Val Ile Arg Gly Gly Ser Phe Leu Cys Asn  
 305 310 315 320

Asp Ser Tyr Cys Ser Gly Tyr Arg Val Ser Arg Arg Met Ser Ser Ser  
 325 330 335

Arg Asp Ser Gly Phe Asn His Thr Gly Phe Arg Cys Val Lys Asp Val  
 340 345 350

Asn Gly

<210> 69  
 <211> 876  
 <212> DNA  
 <213> Pseudomonas putida KT2440

<400> 69  
 atggtgcacg tgccggggcgg cgagttcagc tttggttcaa gccgctttta cgacgaagaa 60  
 ggccccgctc accccgcca ggtgtccggc ttctggattg acgtgcatcc ggtcaccaac 120  
 gccagttcg cgcgcttcgt caaggccacg gggatatgtca cccatgccga gcgcggtacc 180  
 cgtgtcgagg acgaccctgc cctgcccgcac gcgctgcgga taccgggtgc gatggtgttt 240



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catcaggggtg cggacgtgct cggccccggc tggcagttcg tgcccggcgc caactggcga      300
caccgcgaag ggccgggcag cagcctggcc gggctggaca accatccggt ggtgcagatc      360
gccctggaag atgcccaggc ctatgcccgc tgggcaggcc gcgaactgcc cagcgaggcg      420
cagctggaat acgccatgcg cggcggcctg accgatgccg acttcagctg gggtagacc      480
gagcagccca agggcaagct catggccaat acctggcagg gtcagttccc ttatcgcaat      540
gcggcgaagg atggttttac cggtagatcg cccgtggggtt gcttcccggc caacggcttt      600
ggcctgttcg atgccggcgg caatgtctgg gagctgactc gcacgggcta tcggccaggc      660
catgacgcac agcgcgacgc caagctcgac ccctcaggcc cggccctgag tgacagcttc      720
gacccggcag accccggcgt gccgggtggcg gtaatcaaag gcggctcgca cctgtgttcg      780
gcggaccgct gcatgcgcta ccgcccctcg gcacgccagc cgcagccggt gttcatgacg      840
acctcgcacg tgggtttcag aacgattcgg caatga      876

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<210> 70
<211> 291
<212> PRT
<213> Pseudomonas putida KT2440

```

```
<400> 70
```

```

Met Val His Val Pro Gly Gly Glu Phe Ser Phe Gly Ser Ser Arg Phe
1           5           10           15

```

```

Tyr Asp Glu Glu Gly Pro Pro His Pro Ala Lys Val Ser Gly Phe Trp
          20           25           30

```

```

Ile Asp Val His Pro Val Thr Asn Ala Gln Phe Ala Arg Phe Val Lys
          35           40           45

```

```

Ala Thr Gly Tyr Val Thr His Ala Glu Arg Gly Thr Arg Val Glu Asp
          50           55           60

```

```

Asp Pro Ala Leu Pro Asp Ala Leu Arg Ile Pro Gly Ala Met Val Phe
65           70           75           80

```

```

His Gln Gly Ala Asp Val Leu Gly Pro Gly Trp Gln Phe Val Pro Gly
          85           90           95

```

```

Ala Asn Trp Arg His Pro Gln Gly Pro Gly Ser Ser Leu Ala Gly Leu
          100          105          110

```

Asp Asn His Pro Val Val Gln Ile Ala Leu Glu Asp Ala Gln Ala Tyr  
 115 120 125

Ala Arg Trp Ala Gly Arg Glu Leu Pro Ser Glu Ala Gln Leu Glu Tyr  
 130 135 140

Ala Met Arg Gly Gly Leu Thr Asp Ala Asp Phe Ser Trp Gly Thr Thr  
 145 150 155 160

Glu Gln Pro Lys Gly Lys Leu Met Ala Asn Thr Trp Gln Gly Gln Phe  
 165 170 175

Pro Tyr Arg Asn Ala Ala Lys Asp Gly Phe Thr Gly Thr Ser Pro Val  
 180 185 190

Gly Cys Phe Pro Ala Asn Gly Phe Gly Leu Phe Asp Ala Gly Gly Asn  
 195 200 205

Val Trp Glu Leu Thr Arg Thr Gly Tyr Arg Pro Gly His Asp Ala Gln  
 210 215 220

Arg Asp Ala Lys Leu Asp Pro Ser Gly Pro Ala Leu Ser Asp Ser Phe  
 225 230 235 240

Asp Pro Ala Asp Pro Gly Val Pro Val Ala Val Ile Lys Gly Gly Ser  
 245 250 255

His Leu Cys Ser Ala Asp Arg Cys Met Arg Tyr Arg Pro Ser Ala Arg  
 260 265 270

Gln Pro Gln Pro Val Phe Met Thr Thr Ser His Val Gly Phe Arg Thr  
 275 280 285

Ile Arg Gln  
 290

<210> 71  
 <211> 780  
 <212> DNA  
 <213> Ralstonia metallidurans

<400> 71  
 atgggtcgcg gcgggatggt gttcgtcggc accaacagcc cggtgccgct gcgcgaatac

```

tggcgctggt ggcgcttcgt acctggcgcg gactggcgctc acccgaccgg cccgggcagt 120
tccatcgaag gcaaggacaa tcattcccgtc gtgcaggtct cgtatgaaga cgcgcaggcg 180
tacgccaagt gggccggcaa gcgtctgccc accgaggccg agtgggagtt tgccgcccg 240
ggcggcctgg agcaggccac ctacgcctgg ggtgacaagt tcgcgccgga tggccggcag 300
atggcgaatg tctggcaggg ccagcaggtg cagccgttcc cggtggtcag cgccaaggcg 360
ggcggcgcgg ctggcaccag tgctgtcggc acgttcccgg gcaatggcta tgggctctat 420
gacatgaccg gcaacgcctg gcagtgggtg gccgactggt atcgcgcgga ccagttccgc 480
cgcgaagcca cggtggcggc agtgctgcag aatccgaccg gcccggccga ttcgtgggac 540
ccgaccgaac ctggcggtgcc ggtgtcggcg cccaagcggg tcacgcgcgg tggctcgttc 600
ctctgcaacg aggacttctg cctcagctac cggccgagtg cccggcgcgg taccgaccgg 660
tacaccagca tgtcgcacct aggcttccgg ctctgatg atgacgcccg ttgggcagaa 720
gttcgcaagc agccagccgt ggcaatggcc gcgggcgggc agcagaacgt gcagaaataa 780

```

```

<210> 72
<211> 259
<212> PRT
<213> Ralstonia metallidurans

```

```
<400> 72
```

```

Met Val Ala Gly Gly Met Val Phe Val Gly Thr Asn Ser Pro Val Pro
1           5           10           15

```

```

Leu Arg Glu Tyr Trp Arg Trp Trp Arg Phe Val Pro Gly Ala Asp Trp
          20           25           30

```

```

Arg His Pro Thr Gly Pro Gly Ser Ser Ile Glu Gly Lys Asp Asn His
          35           40           45

```

```

Pro Val Val Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp
          50           55           60

```

```

Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg
65           70           75           80

```

```

Gly Gly Leu Glu Gln Ala Thr Tyr Ala Trp Gly Asp Lys Phe Ala Pro
          85           90           95

```

Asp Gly Arg Gln Met Ala Asn Val Trp Gln Gly Gln Gln Val Gln Pro  
 100 105 110

Phe Pro Val Val Ser Ala Lys Ala Gly Gly Ala Ala Gly Thr Ser Ala  
 115 120 125

Val Gly Thr Phe Pro Gly Asn Gly Tyr Gly Leu Tyr Asp Met Thr Gly  
 130 135 140

Asn Ala Trp Gln Trp Val Ala Asp Trp Tyr Arg Ala Asp Gln Phe Arg  
 145 150 155 160

Arg Glu Ala Thr Val Ala Ala Val Leu Gln Asn Pro Thr Gly Pro Ala  
 165 170 175

Asp Ser Trp Asp Pro Thr Glu Pro Gly Val Pro Val Ser Ala Pro Lys  
 180 185 190

Arg Val Thr Arg Gly Gly Ser Phe Leu Cys Asn Glu Asp Phe Cys Leu  
 195 200 205

Ser Tyr Arg Pro Ser Ala Arg Arg Gly Thr Asp Pro Tyr Thr Ser Met  
 210 215 220

Ser His Leu Gly Phe Arg Leu Val Met Asp Asp Ala Arg Trp Ala Glu  
 225 230 235 240

Val Arg Lys Gln Pro Ala Val Ala Met Ala Ala Gly Gly Gln Gln Asn  
 245 250 255

Val Gln Lys

<210> 73

<211> 876

<212> DNA

<213> Prochlorococcus marinus

<400> 73

gtgaccacat ctttgccagt agagatggta accatccccg cagggctcta tcgagttggc 60

tgtgatcgct gctatccgga tggttcagtt cgctgctatc cggaggaaac acccgcgcca 120

gaagtgcagc ttgactcatt ccagatcgac gtagggccag tcaccaatgc ccagttccga 180

gctttcggtta gcgccacgca gcatctcaca gtctcggagc taccaccta tccaacgctc 240

tatcccgatc tagcgcccgga ggaacgcac cctgaatcag ttgtctttca accgcctcca 300  
 gcaacggtgg atcgacagcaa acccttgagc tgggtggaccc tcatggctgg ggctgattgg 360  
 cgtcatcccc aaggacccga aagcacgac gatggccttg atgatcacc tgctgtgcat 420  
 gtcgcctatg ccgacgccat cgcctatgcc cattgggctg gcaagcgtct cccctctgct 480  
 gaagagtggg aagtagccgc ccgcgggggt cttgtcgatg cccaatacgc ctgggggaat 540  
 gaactcactc ccaataaccg ctggatggcg aacatctggc aaggtccttt cccttggcac 600  
 aacgaggagc tagacggctg gttctggacc tcgcccgttg gcagctttcc tgccaacggc 660  
 tatggactct tggatgtttg cggcaatgtg tgggaatgga ccaactctgt ttatcccgctg 720  
 gcgtcaggcc accaggaacg gcgaactatc aaaggcggat cgtttctctg cgcagataat 780  
 tactgcgtac gttatcgacc ctctgcacta caaggccaga cagtagacac tgccacctgt 840  
 cacatgggct ttcgctgtgc aaaaggaggg ccttga 876

<210> 74  
 <211> 291  
 <212> PRT  
 <213> *Prochlorococcus marinus*

<400> 74

Met Thr Thr Ser Leu Pro Val Glu Met Val Thr Ile Pro Ala Gly Leu  
 1 5 10 15

Tyr Arg Val Gly Cys Asp Arg Cys Tyr Pro Asp Gly Ser Val Arg Cys  
 20 25 30

Tyr Pro Glu Glu Thr Pro Ala Arg Glu Val Gln Leu Asp Ser Phe Gln  
 35 40 45

Ile Asp Val Gly Pro Val Thr Asn Ala Gln Phe Arg Ala Phe Val Ser  
 50 55 60

Ala Thr Gln His Leu Thr Val Ser Glu Leu Pro Pro Asp Pro Thr Leu  
 65 70 75 80

Tyr Pro Asp Leu Ala Pro Glu Glu Arg Ile Pro Glu Ser Val Val Phe  
 85 90 95

Gln Pro Pro Pro Ala Thr Val Asp Arg Ser Lys Pro Leu Ser Trp Trp  
 100 105 110

Thr Leu Met Ala Gly Ala Asp Trp Arg His Pro Gln Gly Pro Glu Ser  
 115 120 125

Thr Ile Asp Gly Leu Asp Asp His Pro Val Val His Val Ala Tyr Ala  
 130 135 140

Asp Ala Ile Ala Tyr Ala His Trp Ala Gly Lys Arg Leu Pro Ser Ala  
 145 150 155 160

Glu Glu Trp Glu Val Ala Ala Arg Gly Gly Leu Val Asp Ala Gln Tyr  
 165 170 175

Ala Trp Gly Asn Glu Leu Thr Pro Asn Asn Arg Trp Met Ala Asn Ile  
 180 185 190

Trp Gln Gly Pro Phe Pro Trp His Asn Glu Glu Leu Asp Gly Trp Phe  
 195 200 205

Trp Thr Ser Pro Val Gly Ser Phe Pro Ala Asn Gly Tyr Gly Leu Leu  
 210 215 220

Asp Val Cys Gly Asn Val Trp Glu Trp Thr Asn Ser Val Tyr Pro Val  
 225 230 235 240

Ala Ser Gly His Gln Glu Arg Arg Thr Ile Lys Gly Gly Ser Phe Leu  
 245 250 255

Cys Ala Asp Asn Tyr Cys Val Arg Tyr Arg Pro Ser Ala Leu Gln Gly  
 260 265 270

Gln Thr Val Asp Thr Ala Thr Cys His Met Gly Phe Arg Cys Ala Lys  
 275 280 285

Gly Gly Pro  
 290

<210> 75  
 <211> 1017  
 <212> DNA  
 <213> *Caulobacter crescentus* CB15

<400> 75  
 ttgggaaac tgacggcgct tcccgctctg atgcttctgg cgctggccgg ctgcggccag

ccggcgccca aggcttgctt ggcggacctg ccggttccag atccccagaa ccgcacggcg 120  
 ggtatggttc ggctggcggg cggcgacttc cagatgggcg ctgcgccgct gcgtccggag 180  
 gagggaccgc cccagacggt cacgggtccc cegtcttctgga tcgatcagac agaggtcacc 240  
 aacgccgcct tcgcgcgggt cgtcgaggcc acgggttatc gcaccgtggc cgagcgaccg 300  
 ctcgaccccg cgcgctacgc ccacgtaccg gcggcgcgag ggctccggc ctcgctcgtc 360  
 ttcgtggggg cgaagggggc gaggtcggac gatccttccc aatggtggca ggtgatcccc 420  
 ggcgccgact ggcggcatcc cgaaggtccc ggctcgaaca tccggggcag ggacgcctgg 480  
 ccggtggtgc atatcgctg ggaggacgcc atggcctacg cccgctggct gggccgtgac 540  
 ctgcccacag aggccgaatg ggagtacgcc gcgcgcggcg ggctggttgg caagcgctac 600  
 acctggggcg accaggctca ggatcctgca aagccgcgcg ccaatacttg gcaaggcgctg 660  
 ttcccggccc aggaccttgg caatgacggc ttcaaggcca agcccgcgcc ggtcggctgc 720  
 ttcccgccca acggctatgg cctgcgcgac atggccggca atgtctggga gtggaccgcg 780  
 gactggttca agccgggcct ggatccggtc agcgtcctcg aaaccggcgg gccgcccag 840  
 gcccgcgcg cggatcccga ggaccgaac acgccaagc acgtcgtgaa gggcggttcg 900  
 ttctgtgcg ccgacgacta ctgcttccgc tatcgacctg cggcgcgaa gccggggccg 960  
 ccggacagcg gcgcatcgca tgtcggtttc cgcaccgtgc tccgcgccga gcgctga 1017

<210> 76  
 <211> 338  
 <212> PRT  
 <213> *Caulobacter crescentus* CB15

<400> 76

Met Gly Lys Leu Thr Ala Leu Pro Val Leu Met Leu Leu Ala Leu Ala  
 1 5 10 15

Gly Cys Gly Gln Pro Ala Pro Lys Ala Cys Leu Ala Asp Leu Pro Val  
 20 25 30

Pro Asp Pro Gln Asn Arg Thr Ala Gly Met Val Arg Leu Ala Gly Gly  
 35 40 45

Asp Phe Gln Met Gly Ala Ala Pro Leu Arg Pro Glu Glu Gly Pro Pro  
 50 55 60

Gln Thr Val Thr Val Pro Pro Phe Trp Ile Asp Gln Thr Glu Val Thr  
65 70 75 80

Asn Ala Ala Phe Ala Arg Phe Val Glu Ala Thr Gly Tyr Arg Thr Val  
85 90 95

Ala Glu Arg Pro Leu Asp Pro Ala Arg Tyr Ala His Val Pro Ala Ala  
100 105 110

Gln Arg Arg Pro Ala Ser Leu Val Phe Val Gly Ala Lys Gly Ala Arg  
115 120 125

Ser Asp Asp Pro Ser Gln Trp Trp Gln Val Ile Pro Gly Ala Asp Trp  
130 135 140

Arg His Pro Glu Gly Pro Gly Ser Asn Ile Arg Gly Arg Asp Ala Trp  
145 150 155 160

Pro Val Val His Ile Ala Trp Glu Asp Ala Met Ala Tyr Ala Arg Trp  
165 170 175

Leu Gly Arg Asp Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg  
180 185 190

Gly Gly Leu Val Gly Lys Arg Tyr Thr Trp Gly Asp Gln Ala Gln Asp  
195 200 205

Pro Ala Lys Pro Arg Ala Asn Thr Trp Gln Gly Val Phe Pro Ala Gln  
210 215 220

Asp Leu Gly Asn Asp Gly Phe Lys Ala Lys Pro Ala Pro Val Gly Cys  
225 230 235 240

Phe Pro Pro Asn Gly Tyr Gly Leu Arg Asp Met Ala Gly Asn Val Trp  
245 250 255

Glu Trp Thr Arg Asp Trp Phe Lys Pro Gly Leu Asp Pro Val Ser Val  
260 265 270

Leu Glu Thr Gly Gly Pro Pro Glu Ala Arg Ala Leu Asp Pro Glu Asp  
275 280 285

Pro Asn Thr Pro Lys His Val Val Lys Gly Gly Ser Phe Leu Cys Ala



290

295

300

Asp Asp Tyr Cys Phe Arg Tyr Arg Pro Ala Ala Arg Thr Pro Gly Pro  
 305 310 315 320

Pro Asp Ser Gly Ala Ser His Val Gly Phe Arg Thr Val Leu Arg Ala  
 325 330 335

Glu Arg

<210> 77

<211> 900

<212> DNA

<213> Mycobacterium tuberculosis H37Rv

<400> 77

gtgctgaccg agttggttga cctgcccggc ggatcggtcc gcatgggctc gacgcgcttc 60  
 taccccaag aagcgccgat tcataccgtg accgtgcgcg cctttgcggt agagcgacac 120  
 ccggtgacca acgcgcaatt tgccgaattc gtctccgcga caggctatgt gacggttgca 180  
 gaacaacccc ttgaccccgg gctctacca ggagtggacg cagcagacct gtgtcccggg 240  
 gcgatggtgt tttgtccgac ggccggggccg gtcgacctgc gtgactggcg gcaatggtgg 300  
 gactgggtac ctggcgccctg ctggcgccat ccgtttggcc gggacagcga tatcgccgac 360  
 cgagccggcc acccggtcgt acagggtggcc tatccggacg ccgtggccta cgcacgatgg 420  
 gctggtcgac gcctaccgac cgaggccgag tgggagtacg cggcccgtgg cggaaccacg 480  
 gcaacctatg cgtggggcga ccaggagaag ccggggggcga tgctcatggc gaacacctgg 540  
 cagggccggt ttccttaccg caacgacggt gcattgggct gggtgggaaac ctccccggtg 600  
 ggcaggtttc cggccaacgg gtttggcttg ctcgacatga tcggaaacgt ttgggagtgg 660  
 accaccaccg agttctatcc acaccatcgc atcgatccac cctcgacggc ctgctgcgca 720  
 ccggtcaagc tcgctacagc cgccgaccg acgatcagcc agaccctcaa gggcggctcg 780  
 cacctgtgcg cgccggagta ctgccaccgc taccgcccgg cggcgcgctc gccgcagtcg 840  
 caggacaccg cgaccacca tatcgggttc cgggtgctgg ccgaccgggt gtccgggtag 900

<210> 78

<211> 299

<212> PRT

<213> Mycobacterium tuberculosis H37Rv

&lt;400&gt; 78

Met Leu Thr Glu Leu Val Asp Leu Pro Gly Gly Ser Phe Arg Met Gly  
 1 5 10 15

Ser Thr Arg Phe Tyr Pro Glu Glu Ala Pro Ile His Thr Val Thr Val  
 20 25 30

Arg Ala Phe Ala Val Glu Arg His Pro Val Thr Asn Ala Gln Phe Ala  
 35 40 45

Glu Phe Val Ser Ala Thr Gly Tyr Val Thr Val Ala Glu Gln Pro Leu  
 50 55 60

Asp Pro Gly Leu Tyr Pro Gly Val Asp Ala Ala Asp Leu Cys Pro Gly  
 65 70 75 80

Ala Met Val Phe Cys Pro Thr Ala Gly Pro Val Asp Leu Arg Asp Trp  
 85 90 95

Arg Gln Trp Trp Asp Trp Val Pro Gly Ala Cys Trp Arg His Pro Phe  
 100 105 110

Gly Arg Asp Ser Asp Ile Ala Asp Arg Ala Gly His Pro Val Val Gln  
 115 120 125

Val Ala Tyr Pro Asp Ala Val Ala Tyr Ala Arg Trp Ala Gly Arg Arg  
 130 135 140

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Thr Thr  
 145 150 155 160

Ala Thr Tyr Ala Trp Gly Asp Gln Glu Lys Pro Gly Gly Met Leu Met  
 165 170 175

Ala Asn Thr Trp Gln Gly Arg Phe Pro Tyr Arg Asn Asp Gly Ala Leu  
 180 185 190

Gly Trp Val Gly Thr Ser Pro Val Gly Arg Phe Pro Ala Asn Gly Phe  
 195 200 205

Gly Leu Leu Asp Met Ile Gly Asn Val Trp Glu Trp Thr Thr Thr Glu  
 210 215 220

Phe Tyr Pro His His Arg Ile Asp Pro Pro Ser Thr Ala Cys Cys Ala  
 225 230 235 240

Pro Val Lys Leu Ala Thr Ala Ala Asp Pro Thr Ile Ser Gln Thr Leu  
 245 250 255

Lys Gly Gly Ser His Leu Cys Ala Pro Glu Tyr Cys His Arg Tyr Arg  
 260 265 270

Pro Ala Ala Arg Ser Pro Gln Ser Gln Asp Thr Ala Thr Thr His Ile  
 275 280 285

Gly Phe Arg Cys Val Ala Asp Pro Val Ser Gly  
 290 295

<210> 79  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> conserved domain in prokaryotes and prokaryotes

<220>  
 <221> MISC\_FEATURE  
 <222> 3, 4  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> 6  
 <223> Gly or Ala

<400> 79

Arg Val Xaa Xaa Gly Xaa Ser  
 1 5

<210> 80  
 <211> 630  
 <212> DNA  
 <213> Oncorhynchus mykiss

<400> 80  
 tcaggtggct gctgccccct ggtggttgcc tgtcagagga gcagactgga ggcaccctga 60  
 gggccccgac tccagcatca cagacaggct ggaccaccct gtgctgcatg tgatcatggca 120  
 ggacgctgtg gcctactgct cctgggccta caagagacta cccacagagg ctgagtggga 180

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gtacgcctgc agagggggcc tacaggagag actttacccg tgggggaaca aactgaaacc 240
taaaggacag cactacgcca acctctggca gggaaagtcc cccacacaca actcagaaga 300
ggacgggtac actaaaacct caccagtga gtcatttctt gcaaattggct atggcctgta 360
caacatggta gggaaatgcat gggagtggac atctgactgg tggactgtac accacaccac 420
agatgaacag cacaacccgg caggtccacc atcaggcaca gaccgagtga agaaaggagg 480
ctcctacatg tgccataagt catactgtta caggtacagg tgtgcagcac ggagtcagaa 540
caccctgac agctctgcct ctaacctagg gttccgctgt gtctcccagg agcagccgta 600
acctttcacc ctgcaccctg acatgggtag 630

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<210> 81
<211> 655
<212> DNA
<213> Danio rerio

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<220>
<221> misc_feature
<222> 590
<223> n is a, c, g, or t

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<220>
<221> misc_feature
<222> 626
<223> n is a, c, g, or t

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<400> 81
caaattggttt tatttacata aaaaaatcct cttagtttga agtgtaagac agtgagatta 60
gtgatgtttg aggttatgga tcaacatcag aggcgcagcg gaagcccaag ttcgaggctg 120
aactgtccgg tgtgttctga ctgcgagcgg cacacctgta tctgtagcag taagacttgt 180
ggcacatgta ggatcctcct ttcttgactc tgtctgtccc tgattctggg ccctttgggt 240
taaacttgtc ttctgcagtg tgatgcacag tccaccagtc tgccgtccac tcccacgcat 300
ttcccacat gtcatacagg ccaaagccat tgggaggaaa agacatcacc ggggatgtgt 360
tggcatagcc gtcctctgca gtgttgtgat tagggaaatc tccctgccac aggttagcat 420
agtgtgccc tcttggcatt aatttatttc cccatgggta catcctgtcc tgtagtcttc 480
ctctacaggc caactcccat tcagcttctg taggaagtct gcgtttggcc cattgacagt 540
acgcccgtgc atcatcccat gaaacatgca gagcaggggtg attcattctn gtgtgtatgg 600
ttgaatctgg tcctttctgg tgtctncagt ctgcaccttt cactggtgac cacca 655

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<210> 82  
 <211> 773  
 <212> DNA  
 <213> *Oryzias latipes*

<220>  
 <221> misc\_feature  
 <222> 690  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> 755  
 <223> n is a, c, g, or t

<400> 82  
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 gagacagtac aaaaaatctg cctttgtaaa attagagtta caaaaatata ttttagattt 120  
 gactttcttca gaattgtcgg tggcagcaaa agaatcggat tgatctcatg acaagagcgt 180  
 gagccagaag ttcttggatc aaactgattt ggttctgtca tcgtttctgt tcagcagcac 240  
 agcgaaaacc aagattggaa gcggagctgt ctggagtgtt ttggcttcga gcagcacatc 300  
 tgtacctgta acaataagac ttgtggcaca tgtacgagcc tcctttcttc accttatctg 360  
 tgcctgacgg aggaccctgt gggttgtgct gatggctctgt tgtgtggtgc acgctccacc 420  
 agtctgaggt cactcccat gcgttcccca ccatgtcata cagacaaaa gcattgcctg 480  
 ggaaggacat caccggggag gtttttagtgt agccatcctc tgcagagttg tgtgctggga 540  
 attccccctg ccagagggtg gcgtaatget gtcccttgg gtttagcttg tttccccagg 600  
 ggtagagtct gtccttcagg ccgcccctgc aggcaacctc cactctgcc tcagtgggaa 660  
 gtctcttggt gaccaggag cagtaagccn aggcattcatt ccagaaaacc tgaacgacgg 720  
 atgatccatc ctgtctgtga tggtggagtc tggancttca gggtgcttcc agt 773

<210> 83  
 <211> 566  
 <212> DNA  
 <213> *Xenopus laevis*

<220>  
 <221> misc\_feature  
 <222> 6  
 <223> n is a, c, g, or t

<220>

<221> misc\_feature  
 <222> 47  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> 81  
 <223> n is a, c, g, or t

<400> 83  
 atatgnaact aaaggtaatg taattggaat gatggatttc acaaggntcg agagttccct 60  
 attgctcctg cttgtcgtgt nacaggtcac ggagccggcg ccacacagcg aaatcccagg 120  
 ttggaggccg agctgtcggg tgtattctga cttcgagcag cacagcgata cctgtagcaa 180  
 taggactcat ggcacatgta ggagcctcct ttcttcactc tatcatttcc cgtagaaggt 240  
 cctttcgggt tgtgaacctc atctgctgta tgatgagtgt cccaccaatc agatgtccac 300  
 tcccaagcat ttcccaccat gttatataga ccataaccat tggctgggaa agcagttaca 360  
 ggtgaagtct gcacataacc atcctctcca gtgttttggg ttggaaaatc cccctgccag 420  
 acattcgcat aatgttgtcc ctttggttcc agcttggtcc cccatggaaa aatcctgttc 480  
 tcaagtcccc cgcggcaggc gtattcccac tcagcttcag ttggaaggcg tttacctgcc 540  
 caggtgcaga aagcagaagc atcatt 566

<210> 84  
 <211> 647  
 <212> DNA  
 <213> *Silurana tropicalis*

<400> 84  
 gccgcttttt tttttttttt tttttttttt catcacaaaa ataattttat taataaaata 60  
 ggattttgtg ttcattctta ttatgaagga caaggaatgt cattgaaatt tttgttttca 120  
 caaggtcttg ggagttcctt cctgctcagg tcattttgca gtggtcacgg agccgacgcc 180  
 acgcagcgga atcccagggt agaggccgag ctgtcaggtg tattctgact tcgagcagca 240  
 cagcgatacc tgtagcagta ggactcatgg cacatgtatg agcctccttt tttcaccttg 300  
 tcttttcccg taaaaggacc tttcgggttg taagtctcat ctgctgtatg atgagtgtcc 360  
 caccaatcgg atgtccactc ccaagcattt cccaccatgt tatataggct ataaccattg 420  
 gctgggaaag cggttacagg tgaagtctgc acatagccgt cctctccagt gttttgggtt 480  
 ggaaattccc cctgccagac attcgcataa tgttctccct ttggttccag cttgttcccc 540  
 cacggaaaaa gcctgttctc aagtccccca cgggaggcat attcccactc agcttctgtc 600

ggaaggcgct tacccgccca ggtgcagaag gcagaagcat cgttcca 647

<210> 85  
 <211> 636  
 <212> DNA  
 <213> Salmo salar

<400> 85  
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 ggtaatcctg catttcatga agaacactga catcactggc tgtatgaaga ggtgcacttg 120  
 atttgtttcg cctggcgggc aagataggca gagtttagcac cctagactag agccaatggc 180  
 gaatgggtaca aaaagggaaa agtcagacta cccatgtcag ggtcaagggc aaaagggttac 240  
 ggctgctcct gggagacaca gcggaaccct aggttagagg cagagctgtc aggggtgttc 300  
 tgactccgtg ctgcacacct gtacctgtaa cagtatgact tatggcacat gtaggagcct 360  
 cctttcttca ctcggtctgt gcctgatggc ggacctgccg ggttgtgccg ttcattctgtg 420  
 gtgtgggtgta cagtccacca gtcagatgtc cactcccatg cattccctac catgttgtac 480  
 aggccatagc catttgcagg aaatgacttc actggtgagg ttttgggtgta cccgtcctct 540  
 tctgagttgt gtgtggggaa ctttcctgtc cagaggttgg cgtagtgtg tccttttaggt 600  
 ttcagtttgt tccccacgg gtaaagtctg tcctgt 636

<210> 86  
 <211> 415  
 <212> DNA  
 <213> Sus scrofa

<400> 86  
 agtttctgt gaccaacacc ggagaggatg gcttccgagg aactgcgcct gttgatgcct 60  
 ttcctcccaa tggttatggc ctttacaata tagtagggaa cgcctgggaa tggacctcag 120  
 actggtggac cattcaccat gctgctgaag aaacaattaa cccatcaagt tcttctgtct 180  
 gcaccgaata acagagccgc cactacgtga tgaaagcaga gaaaggcccc ctttctggga 240  
 aagaccgggt gaagaaaggg ggatcctata tgtgccataa gtcctactgc tacagggtacc 300  
 gctgtgtgtc tcgaagccag aacacgccgg acagctcggc ttcaaactctg gggttccgct 360  
 gtgcagctga ccaccagccc accacaggct gagtcaggaa gagtcttccc gaatc 415

<210> 87  
 <211> 595  
 <212> DNA  
 <213> Bos taurus

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<400> 87
ccacgcgtcc gggggcaaca aactgcagcc gaaaggccag cattatagcc aacatcttgg      60
caaggcgagt ttcctgtgac caacaccggg gaggacggct tccgaggac cgcgcctgtt      120
gacgcctttc ctcccaatgg ttattggctt atacaatata gtagggaacg cctgggagtg      180
gacttcagac tgggtggactg ttcaccattc tgctgaagaa acgattaacc caaaaggccc      240
cccttctggg aaagaccggg tgaagaaagg tggatcctac atgtgccata aatcctattg      300
ctacaggtat cgctgtgctg ctcgaagcca gaacacaccc gacagctctg cttcgaatct      360
gggattccgt tgtgcagctg accacctgcc caccacaggc taagagccaa aaagagcctt      420
cccgaaccgg agaagtcgtg tctactctgc acgcggtctc cctcagaagg ctgaacaacc      480
tgctgtgaag aattcccacc ccaaggtggg ttacatacct tgcccagtgg ccaaaggacc      540
tatggcaaga ccaaattgct gagctgatca gcatgtgcgc tttattgggg gatgg      595

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<210> 88
<211> 1611
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1608)

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<400> 88
atg cta ctg ctg tgg gtg tcg gtg gtc gca gcc ttg gcg ctg gcg gta      48
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val
1          5          10          15

ctg gcc ccc gga gca ggg gag cag agg cgg aga gca gcc aaa gcg ccc      96
Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro
20          25          30

aat gtg gtg ctg gtc gtg agc gac tcc ttc gat gga agg tta aca ttt      144
Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe
35          40          45

cat cca gga agt cag gta gtg aaa ctt cct ttt atc aac ttt atg aag      192
His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys
50          55          60

aca cgt ggg act tcc ttt ctg aat gcc tac aca aac tct cca att tgt      240
Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys
65          70          75          80

tgc cca tca cgc gca gca atg tgg agt ggc ctc ttc act cac tta aca      288
Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr
85          90          95

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gaa tct tgg aat aat ttt aag ggt cta gat cca aat tat aca aca tgg	336
Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp	
100 105 110	
atg gat gtc atg gag agg cat ggc tac cga aca cag aaa ttt ggg aaa	384
Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys	
115 120 125	
ctg gac tat act tca gga cat cac tcc att agt aat cgt gtg gaa gcg	432
Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala	
130 135 140	
tgg aca aga gat gtt gct ttc tta ctc aga caa gaa ggc agg ccc atg	480
Trp Thr Arg Asp Val Ala Phe Leu Leu Arg Gln Glu Gly Arg Pro Met	
145 150 155 160	
gtt aat ctt atc cgt aac agg act aaa gtc aga gtg atg gaa agg gat	528
Val Asn Leu Ile Arg Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp	
165 170 175	
tgg cag aat aca gac aaa gca gta aac tgg tta aga aag gaa gca att	576
Trp Gln Asn Thr Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile	
180 185 190	
aat tac act gaa cca ttt gtt att tac ttg gga tta aat tta cca cac	624
Asn Tyr Thr Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His	
195 200 205	
cct tac cct tca cca tct tct gga gaa aat ttt gga tct tca aca ttt	672
Pro Tyr Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe	
210 215 220	
cac aca tct ctt tat tgg ctt gaa aaa gtg tct cat gat gcc atc aaa	720
His Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	
225 230 235 240	
atc cca aag tgg tca cct ttg tca gaa atg cac cct gta gat tat tac	768
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr Tyr	
245 250 255	
tct tct tat aca aaa aac tgc act gga aga ttt aca aaa aaa gaa att	816
Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys Glu Ile	
260 265 270	
aag aat att aga gca ttt tat tat gct atg tgt gct gag aca gat gcc	864
Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu Thr Asp Ala	
275 280 285	
atg ctt ggt gaa att att ttg gcc ctt cat caa tta gat ctt ctt cag	912
Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu Asp Leu Leu Gln	
290 295 300	
aaa act att gtc ata tac tcc tca gac cat gga gag ctg gcc atg gaa	960
Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly Glu Leu Ala Met Glu	
305 310 315 320	

cat cga cag ttt tat aaa atg agc atg tac gag gct agt gca cat gtt	1008
His Arg Gln Phe Tyr Lys Met Ser Met Tyr Glu Ala Ser Ala His Val	
325 330 335	
ccg ctt ttg atg atg gga cca gga att aaa gcc ggc cta caa gta tca	1056
Pro Leu Leu Met Met Gly Pro Gly Ile Lys Ala Gly Leu Gln Val Ser	
340 345 350	
aat gtg gtt tct ctt gtg gat att tac cct acc atg ctt gat att gct	1104
Asn Val Val Ser Leu Val Asp Ile Tyr Pro Thr Met Leu Asp Ile Ala	
355 360 365	
gga att cct ctg cct cag aac ctg agt gga tac tct ttg ttg ccg tta	1152
Gly Ile Pro Leu Pro Gln Asn Leu Ser Gly Tyr Ser Leu Leu Pro Leu	
370 375 380	
tca tca gaa aca ttt aag aat gaa cat aaa gtc aaa aac ctg cat cca	1200
Ser Ser Glu Thr Phe Lys Asn Glu His Lys Val Lys Asn Leu His Pro	
385 390 395 400	
ccc tgg att ctg agt gaa ttc cat gga tgt aat gtg aat gcc tcc acc	1248
Pro Trp Ile Leu Ser Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr	
405 410 415	
tac atg ctt cga act aac cac tgg aaa tat ata gcc tat tcg gat ggt	1296
Tyr Met Leu Arg Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly	
420 425 430	
gca tca ata ttg cct caa ctc ttt gat ctt tcc tcg gat cca gat gaa	1344
Ala Ser Ile Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu	
435 440 445	
tta aca aat gtt gct gta aaa ttt cca gaa att act tat tct ttg gat	1392
Leu Thr Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp	
450 455 460	
cag aag ctt cat tcc att ata aac tac cct aaa gtt tct gct tct gtc	1440
Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val	
465 470 475 480	
cac cag tat aat aaa gag cag ttt atc aag tgg aaa caa agt ata gga	1488
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly	
485 490 495	
cag aat tat tca aac gtt ata gca aat ctt agg tgg cac caa gac tgg	1536
Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp	
500 505 510	
cag aag gaa cca agg aag tat gaa aat gca att gat cag tgg ctt aaa	1584
Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys	
515 520 525	
acc cat atg aat cca aga gca gtt tga	1611
Thr His Met Asn Pro Arg Ala Val	
530 535	

<210> 89  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 89

Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val  
 1 5 10 15

Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro  
 20 25 30

Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe  
 35 40 45

His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys  
 50 55 60

Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys  
 65 70 75 80

Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr  
 85 90 95

Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp  
 100 105 110

Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys  
 115 120 125

Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala  
 130 135 140

Trp Thr Arg Asp Val Ala Phe Leu Leu Arg Gln Glu Gly Arg Pro Met  
 145 150 155 160

Val Asn Leu Ile Arg Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp  
 165 170 175

Trp Gln Asn Thr Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile  
 180 185 190

Asn Tyr Thr Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His  
 195 200 205

Pro Tyr Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe  
 210 215 220

His Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys  
 225 230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr Tyr  
 245 250 255

Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys Glu Ile  
 260 265 270

Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu Thr Asp Ala  
 275 280 285

Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu Asp Leu Leu Gln  
 290 295 300

Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly Glu Leu Ala Met Glu  
 305 310 315 320

His Arg Gln Phe Tyr Lys Met Ser Met Tyr Glu Ala Ser Ala His Val  
 325 330 335

Pro Leu Leu Met Met Gly Pro Gly Ile Lys Ala Gly Leu Gln Val Ser  
 340 345 350

Asn Val Val Ser Leu Val Asp Ile Tyr Pro Thr Met Leu Asp Ile Ala  
 355 360 365

Gly Ile Pro Leu Pro Gln Asn Leu Ser Gly Tyr Ser Leu Leu Pro Leu  
 370 375 380

Ser Ser Glu Thr Phe Lys Asn Glu His Lys Val Lys Asn Leu His Pro  
 385 390 395 400

Pro Trp Ile Leu Ser Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr  
 405 410 415

Tyr Met Leu Arg Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly  
 420 425 430

Ala Ser Ile Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu  
 435 440 445

Leu Thr Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp  
 450 455 460

Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val  
 465 470 475 480

His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly  
 485 490 495

Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp  
 500 505 510

Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys  
 515 520 525

Thr His Met Asn Pro Arg Ala Val  
 530 535

<210> 90  
 <211> 1722  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1719)

<400> 90  
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 1 5 10 15  
 tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta 96  
 Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu  
 20 25 30  
 cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc 144  
 Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser  
 35 40 45  
 cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat 192  
 Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 50 55 60  
 gtg ggt tac cac gga tct gag att aaa aca cct act ctt gac aag ctc 240

Val 65	Gly	Tyr	His	Gly	Ser 70	Glu	Ile	Lys	Thr	Pro 75	Thr	Leu	Asp	Lys	Leu 80	
gct	gcc	gaa	gga	gtt	aaa	ctg	gag	aac	tac	tat	gtc	cag	cct	att	tgc	288
Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	Ile	Cys	
				85					90					95		
aca	cca	tcc	agg	agt	cag	ttt	att	act	gga	aag	tat	cag	ata	cac	acc	336
Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	Ile	His	Thr	
			100					105					110			
gga	ctt	caa	cat	tct	atc	ata	aga	cct	acc	caa	ccc	aac	tgt	tta	cct	384
Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	Asn	Cys	Leu	Pro	
		115					120					125				
ctg	gac	aat	gcc	acc	cta	cct	cag	aaa	ctg	aag	gag	gtt	gga	tat	tca	432
Leu	Asp	Asn	Ala	Thr	Leu	Pro	Gln	Lys	Leu	Lys	Glu	Val	Gly	Tyr	Ser	
	130					135					140					
acg	cat	atg	gtc	gga	aaa	tgg	cac	ttg	ggt	ttt	tac	aga	aaa	gaa	tgc	480
Thr	His	Met	Val	Gly	Lys	Trp	His	Leu	Gly	Phe	Tyr	Arg	Lys	Glu	Cys	
145					150				155					160		
atg	ccc	acc	aga	aga	gga	ttt	gat	acc	ttt	ttt	ggt	tcc	ctt	ttg	gga	528
Met	Pro	Thr	Arg	Arg	Gly	Phe	Asp	Thr	Phe	Phe	Gly	Ser	Leu	Leu	Gly	
				165				170					175			
agt	ggg	gat	tac	tat	aca	cac	tac	aaa	tgt	gac	agt	cct	ggg	atg	tgt	576
Ser	Gly	Asp	Tyr	Tyr	Thr	His	Tyr	Lys	Cys	Asp	Ser	Pro	Gly	Met	Cys	
			180					185					190			
ggc	tat	gac	ttg	tat	gaa	aac	gac	aat	gct	gcc	tgg	gac	tat	gac	aat	624
Gly	Tyr	Asp	Leu	Tyr	Glu	Asn	Asp	Asn	Ala	Ala	Trp	Asp	Tyr	Asp	Asn	
		195				200						205				
ggc	ata	tac	tcc	aca	cag	atg	tac	act	cag	aga	gta	cag	caa	atc	tta	672
Gly	Ile	Tyr	Ser	Thr	Gln	Met	Tyr	Thr	Gln	Arg	Val	Gln	Gln	Ile	Leu	
	210					215					220					
gct	tcc	cat	aac	ccc	aca	aag	cct	ata	ttt	tta	tat	att	gcc	tat	caa	720
Ala	Ser	His	Asn	Pro	Thr	Lys	Pro	Ile	Phe	Leu	Tyr	Ile	Ala	Tyr	Gln	
225				230				235						240		
gct	gtt	cat	tca	cca	ctg	caa	gct	cct	ggc	agg	tat	ttc	gaa	cac	tac	768
Ala	Val	His	Ser	Pro	Leu	Gln	Ala	Pro	Gly	Arg	Tyr	Phe	Glu	His	Tyr	
				245				250					255			
cga	tcc	att	atc	aac	ata	aac	agg	agg	aga	tat	gct	gcc	atg	ctt	tcc	816
Arg	Ser	Ile	Ile	Asn	Ile	Asn	Arg	Arg	Arg	Tyr	Ala	Ala	Met	Leu	Ser	
			260				265					270				
tgc	tta	gat	gaa	gca	atc	aac	aac	gtg	aca	ttg	gct	cta	aag	act	tat	864
Cys	Leu	Asp	Glu	Ala	Ile	Asn	Asn	Val	Thr	Leu	Ala	Leu	Lys	Thr	Tyr	
		275				280					285					
ggt	ttc	tat	aac	aac	agc	att	atc	att	tac	tct	tca	gat	aat	ggt	ggc	912
Gly	Phe	Tyr	Asn	Asn	Ser	Ile	Ile	Ile	Tyr	Ser	Ser	Asp	Asn	Gly	Gly	

290	295	300	
cag cct acg gca gga ggg agt aac tgg cct ctc aga ggt agc aaa gga Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly 305 310 315 320			960
aca tat tgg gaa gga ggg atc cgg gct gta ggc ttt gtg cat agc cca Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro 325 330 335			1008
ctt ctg aaa aac aag gga aca gtg tgt aag gaa ctt gtg cac atc act Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr 340 345 350			1056
gac tgg tac ccc act ctc att tca ctg gct gaa gga cag att gat gag Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu 355 360 365			1104
gac att caa cta gat ggc tat gat atc tgg gag acc ata agt gag ggt Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly 370 375 380			1152
ctt cgc tca ccc cga gta gat att ttg cat aac att gac ccc ata tac Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr 385 390 395 400			1200
acc aag gca aaa aat ggc tcc tgg gca gca ggc tat ggg atc tgg aac Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn 405 410 415			1248
act gca atc cag tca gcc atc aga gtg cag cac tgg aaa ttg ctt aca Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr 420 425 430			1296
gga aat cct ggc tac agc gac tgg gtc ccc cct cag tct ttc agc aac Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn 435 440 445			1344
ctg gga ccg aac cgg tgg cac aat gaa cgg atc acc ttg tca act ggc Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly 450 455 460			1392
aaa agt gta tgg ctt ttc aac atc aca gcc gac cca tat gag agg gtg Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val 465 470 475 480			1440
gac cta tct aac agg tat cca gga atc gtg aag aag ctc cta cgg agg Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg 485 490 495			1488
ctc tca cag ttc aac aaa act gca gtg ccg gtc agg tat ccc ccc aaa Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys 500 505 510			1536
gac ccc aga agt aac cct agg ctc aat gga ggg gtc tgg gga cca tgg Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp 515 520 525			1584

tat aaa gag gaa acc aag aaa aag aag cca agc aaa aat cag gct gag 1632  
 Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu  
 530 535 540

aaa aag caa aag aaa agc aaa aaa aag aag aag aaa cag cag aaa gca 1680  
 Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala  
 545 550 555 560

gtc tca ggt tca act tgc cat tca ggt gtt act tgt gga taa 1722  
 Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly  
 565 570

<210> 91  
 <211> 573  
 <212> PRT  
 <213> Homo sapiens

<400> 91

Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly  
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Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu  
 20 25 30

Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser  
 35 40 45

Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 50 55 60

Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu  
 65 70 75 80

Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys  
 85 90 95

Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr  
 100 105 110

Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro  
 115 120 125

Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser  
 130 135 140



Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys  
 145 150 155 160

Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly  
 165 170 175

Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys  
 180 185 190

Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn  
 195 200 205

Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu  
 210 215 220

Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln  
 225 230 235 240

Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr  
 245 250 255

Arg Ser Ile Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser  
 260 265 270

Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr  
 275 280 285

Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly  
 290 295 300

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly  
 305 310 315 320

Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro  
 325 330 335

Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr  
 340 345 350

Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu  
 355 360 365

Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly

370

375

380

Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr  
 385 390 395 400

Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn  
 405 410 415

Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr  
 420 425 430

Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn  
 435 440 445

Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly  
 450 455 460

Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val  
 465 470 475 480

Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg  
 485 490 495

Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys  
 500 505 510

Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp  
 515 520 525

Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu  
 530 535 540

Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala  
 545 550 555 560

Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly  
 565 570

<210> 92  
 <211> 1710  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1707)

&lt;400&gt; 92

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Met	His	Thr	Leu	Thr	Gly	Phe	Ser	Leu	Val	Ser	Leu	Leu	Ser	Phe	Gly	
1				5					10					15		

tac	ctg	tcc	tgg	gac	tgg	gcc	aag	ccg	agc	ttc	gtg	gcc	gac	ggg	ccc	96
Tyr	Leu	Ser	Trp	Asp	Trp	Ala	Lys	Pro	Ser	Phe	Val	Ala	Asp	Gly	Pro	
			20					25					30			

ggg	gag	gct	ggc	gag	cag	ccc	tcg	gcc	gct	ccg	ccc	cag	cct	ccc	cac	144
Gly	Glu	Ala	Gly	Glu	Gln	Pro	Ser	Ala	Ala	Pro	Pro	Gln	Pro	Pro	His	
		35					40					45				

atc	atc	ttc	atc	ctc	acg	gac	gac	caa	ggc	tac	cac	gac	gtg	ggc	tac	192
Ile	Ile	Phe	Ile	Leu	Thr	Asp	Asp	Gln	Gly	Tyr	His	Asp	Val	Gly	Tyr	
	50					55					60					

cat	ggt	tca	gat	atc	gag	acc	cct	acg	ctg	gac	agg	ctg	gcg	gcc	aag	240
His	Gly	Ser	Asp	Ile	Glu	Thr	Pro	Thr	Leu	Asp	Arg	Leu	Ala	Ala	Lys	
65					70					75					80	

ggg	gtc	aag	ttg	gag	aat	tat	tac	atc	cag	ccc	atc	tgc	acg	cct	tcg	288
Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Ile	Gln	Pro	Ile	Cys	Thr	Pro	Ser	
				85					90					95		

cgg	agc	cag	ctc	ctc	act	ggc	agg	tac	cag	atc	cac	aca	gga	ctc	cag	336
Arg	Ser	Gln	Leu	Leu	Thr	Gly	Arg	Tyr	Gln	Ile	His	Thr	Gly	Leu	Gln	
			100					105					110			

cat	tcc	atc	atc	cgc	cca	cag	cag	ccc	aac	tgc	ctg	ccc	ctg	gac	cag	384
His	Ser	Ile	Ile	Arg	Pro	Gln	Gln	Pro	Asn	Cys	Leu	Pro	Leu	Asp	Gln	
		115					120					125				

gtg	aca	ctg	cca	cag	aag	ctg	cag	gag	gca	ggt	tat	tcc	acc	cat	atg	432
Val	Thr	Leu	Pro	Gln	Lys	Leu	Gln	Glu	Ala	Gly	Tyr	Ser	Thr	His	Met	
	130					135					140					

gtg	ggc	aag	tgg	cac	ctg	ggc	ttc	tac	cgg	aag	gag	tgt	ctg	ccc	acc	480
Val	Gly	Lys	Trp	His	Leu	Gly	Phe	Tyr	Arg	Lys	Glu	Cys	Leu	Pro	Thr	
145					150					155					160	

cgt	cgg	ggc	ttc	gac	acc	ttc	ctg	ggc	tcg	ctc	acg	ggc	aat	gtg	gac	528
Arg	Arg	Gly	Phe	Asp	Thr	Phe	Leu	Gly	Ser	Leu	Thr	Gly	Asn	Val	Asp	
				165					170					175		

tat	tac	acc	tat	gac	aac	tgt	gat	ggc	cca	ggc	gtg	tgc	ggc	ttc	gac	576
Tyr	Tyr	Thr	Tyr	Asp	Asn	Cys	Asp	Gly	Pro	Gly	Val	Cys	Gly	Phe	Asp	
			180					185					190			

ctg	cac	gag	ggt	gag	aat	gtg	gcc	tgg	ggg	ctc	agc	ggc	cag	tac	tcc	624
Leu	His	Glu	Gly	Glu	Asn	Val	Ala	Trp	Gly	Leu	Ser	Gly	Gln	Tyr	Ser	
		195					200						205			

act atg ctt tac gcc cag cgc gcc agc cat atc ctg gcc agc cac agc Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser 210 215 220	672
cct cag cgt ccc ctc ttc ctc tat gtg gcc ttc cag gca gta cac aca Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr 225 230 235 240	720
ccc ctg cag tcc cct cgt gag tac ctg tac cgc tac cgc acc atg ggc Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly 245 250 255	768
aat gtg gcc cgg cgg aag tac gcg gcc atg gtg acc tgc atg gat gag Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu 260 265 270	816
gct gtg cgc aac atc acc tgg gcc ctc aag cgc tac ggt ttc tac aac Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn 275 280 285	864
aac agt gtc atc atc ttc tcc agt gac aat ggt ggc cag act ttc tcg Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser 290 295 300	912
ggg ggc agc aac tgg ccg ctc cga gga cgc aag ggc act tat tgg gaa Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu 305 310 315 320	960
ggt ggc gtg cgg ggc cta ggc ttt gtc cac agt ccc ctg ctc aag cga Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg 325 330 335	1008
aag caa cgg aca agc cgg gca ctg atg cac atc act gac tgg tac ccg Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro 340 345 350	1056
acc ctg gtg ggt ctg gca ggt ggt acc acc tca gca gcc gat ggg cta Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu 355 360 365	1104
gat ggc tac gac gtg tgg ccg gcc atc agc gag ggc cgg gcc tca cca Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro 370 375 380	1152
cgc acg gag atc ctg cac aac att gac cca ctc tac aac cat gcc cag Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln 385 390 395 400	1200
cat ggc tcc ctg gag ggc ggc ttt ggc atc tgg aac acc gcc gtg cag His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln 405 410 415	1248
gct gcc atc cgc gtg ggt gag tgg aag ctg ctg aca gga gac ccc ggc Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly 420 425 430	1296
tat ggc gat tgg atc cca ccg cag aca ctg gcc acc ttc ccg ggt agc	1344

Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser  
 435 440 445  
 tgg tgg aac ctg gaa cga atg gcc agt gtc cgc cag gcc gtg tgg ctc 1392  
 Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu  
 450 455 460  
 ttc aac atc agt gct gac cct tat gaa cgg gag gac ctg gct ggc cag 1440  
 Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln  
 465 470 475 480  
 cgg cct gat gtg gtc cgc acc ctg ctg gct cgc ctg gcc gaa tat aac 1488  
 Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn  
 485 490 495  
 cgc aca gcc atc ccg gta cgc tac cca gct gag aac ccc cgg gct cat 1536  
 Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His  
 500 505 510  
 cct gac ttt aat ggg ggt gct tgg ggg ccc tgg gcc agt gat gag gaa 1584  
 Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu  
 515 520 525  
 gag gag gaa gag gaa ggg agg gct cga agc ttc tcc cgg ggt cgt cgc 1632  
 Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg  
 530 535 540  
 aag aaa aaa tgc aag att tgc aag ctt cga tcc ttt ttc cgt aaa ctc 1680  
 Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu  
 545 550 555 560  
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 Asn Thr Arg Leu Met Ser Gln Arg Ile  
 565

<210> 93  
 <211> 569  
 <212> PRT  
 <213> Homo sapiens

<400> 93

Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly  
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Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro  
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Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His  
 35 40 45

Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr  
 50 55 60

His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys  
65 70 75 80

Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser  
85 90 95

Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln  
100 105 110

His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln  
115 120 125

Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met  
130 135 140

Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr  
145 150 155 160

Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp  
165 170 175

Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp  
180 185 190

Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser  
195 200 205

Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser  
210 215 220

Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr  
225 230 235 240

Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly  
245 250 255

Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu  
260 265 270

Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn  
275 280 285

Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser  
 290 295 300

Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu  
 305 310 315 320

Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg  
 325 330 335

Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro  
 340 345 350

Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu  
 355 360 365

Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro  
 370 375 380

Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln  
 385 390 395 400

His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln  
 405 410 415

Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly  
 420 425 430

Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser  
 435 440 445

Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu  
 450 455 460

Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln  
 465 470 475 480

Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn  
 485 490 495

Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His  
 500 505 510

Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu  
 515 520 525

Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg  
 530 535 540

Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu  
 545 550 555 560

Asn Thr Arg Leu Met Ser Gln Arg Ile  
 565

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 <211> 2067  
 <212> DNA  
 <213> Homo sapiens

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 <221> CDS  
 <222> (1)..(2064)

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 aca gag gta gat tgt ttt gtg gtt gaa tta gga agt cta cac aat cct 96  
 Thr Glu Val Asp Cys Phe Val Val Glu Leu Gly Ser Leu His Asn Pro  
 20 25 30  
 aca cgg aac cca cag cga att ttc acc aag cac gtg gcc acc aag tca 144  
 Thr Arg Asn Pro Gln Arg Ile Phe Thr Lys His Val Ala Thr Lys Ser  
 35 40 45  
 tcc agc tcc aaa tgt cag ctg gac caa ggt gga aaa agc ctg gtc cag 192  
 Ser Ser Ser Lys Cys Gln Leu Asp Gln Gly Gly Lys Ser Leu Val Gln  
 50 55 60  
 tgc att tta ccc aga tct tca aag ctc ctc tca ccc ttg tgt ctc ccc 240  
 Cys Ile Leu Pro Arg Ser Ser Lys Leu Leu Ser Pro Leu Cys Leu Pro  
 65 70 75 80  
 cat ccg tgt gga gct tta ctt ctg tat aga tcc tca gga atc gcc tct 288  
 His Pro Cys Gly Ala Leu Leu Leu Tyr Arg Ser Ser Gly Ile Ala Ser  
 85 90 95  
 gct ctt gct gcc ttt aca gac tcc ctc tct agg agc tgc tgg ctg tca 336  
 Ala Leu Ala Ala Phe Thr Asp Ser Leu Ser Arg Ser Cys Trp Leu Ser  
 100 105 110  
 gtg tcc ctg tgc tgt ttg ttt tgc ggt gtt gat ggc aca ttt atg aca 384  
 Val Ser Leu Cys Cys Leu Phe Cys Gly Val Asp Gly Thr Phe Met Thr



115	120	125	
aga aac gcc aga ccc aac att gtc ctg ctg atg gca gat gac ctt gga Arg Asn Ala Arg Pro Asn Ile Val Leu Leu Met Ala Asp Asp Leu Gly 130 135 140			432
gtg ggg gat ttg tgc tgc tac ggt aat aac tca gtg agc aca cct aat Val Gly Asp Leu Cys Cys Tyr Gly Asn Asn Ser Val Ser Thr Pro Asn 145 150 155 160			480
att gac cgc ctg gca agt gaa gga gtg agg ctt acc cag cat ctc gca Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala 165 170 175			528
gct gct tcc atg tgc acc cca agt cgg gct gcc ttc ctg acc ggc cgg Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg 180 185 190			576
tac ccc atc aga tca ggg atg gtg tct gcc tac aac ctg aac cgt gcc Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala 195 200 205			624
ttc acg tgg ctt ggt ggg tca ggt ggt ctt ccc acc aat gaa acg act Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr 210 215 220			672
ttt gcc aag ctg ctg cag cac cgt ggc tac cgc acg gga ctc ata ggc Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly 225 230 235 240			720
aaa tgg cac ctg ggt ttg agc tgc gcc tct cgg aat gat cac tgt tac Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr 245 250 255			768
cac ccg ctc aac cat ggt ttt cac tac ttt tac ggg gtg cct ttt gga His Pro Leu Asn His Gly Phe His Tyr Phe Tyr Gly Val Pro Phe Gly 260 265 270			816
ctt tta agc gac tgc cag gca tcc aag aca cca gaa ctg cac cgc tgg Leu Leu Ser Asp Cys Gln Ala Ser Lys Thr Pro Glu Leu His Arg Trp 275 280 285			864
ctc agg atc aaa ctg tgg atc tcc acg gta gcc ctt gcc ctg gtt cct Leu Arg Ile Lys Leu Trp Ile Ser Thr Val Ala Leu Ala Leu Val Pro 290 295 300			912
ttt ctg ctt ctc att ccc aag ttc gcc cgc tgg ttc tca gtg cca tgg Phe Leu Leu Leu Ile Pro Lys Phe Ala Arg Trp Phe Ser Val Pro Trp 305 310 315 320			960
aag gtc atc ttt gtc ttt gct ctc ctc gcc ttt ctg ttt ttc act tcc Lys Val Ile Phe Val Phe Ala Leu Leu Ala Phe Leu Phe Phe Thr Ser 325 330 335			1008
tgg tac tct agt tat gga ttt act cga cgt tgg aat tgc atc ctt atg Trp Tyr Ser Ser Tyr Gly Phe Thr Arg Arg Trp Asn Cys Ile Leu Met 340 345 350			1056

agg aac cat gaa att atc cag cag cca atg aaa gag gag aaa gta gct	1104
Arg Asn His Glu Ile Ile Gln Gln Pro Met Lys Glu Glu Lys Val Ala	
355 360 365	
tcc ctc atg ctg aag gag gca ctt gct ttc att gaa agg tac aaa agg	1152
Ser Leu Met Leu Lys Glu Ala Leu Ala Phe Ile Glu Arg Tyr Lys Arg	
370 375 380	
gaa cct ttt ctc ctc ttt ttt tcc ttc ctg cac gta cat act cca ctc	1200
Glu Pro Phe Leu Leu Phe Phe Ser Phe Leu His Val His Thr Pro Leu	
385 390 395 400	
atc tcc aaa aag aag ttt gtt ggg cgc agt aaa tat ggc agg tat ggg	1248
Ile Ser Lys Lys Lys Phe Val Gly Arg Ser Lys Tyr Gly Arg Tyr Gly	
405 410 415	
gac aat gta gaa gaa atg gat tgg atg gtg ggt aaa atc ctg gat gcc	1296
Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Lys Ile Leu Asp Ala	
420 425 430	
ctg gac cag gag cgc ctg gcc aac cac acc ttg gtg tac ttc acc tct	1344
Leu Asp Gln Glu Arg Leu Ala Asn His Thr Leu Val Tyr Phe Thr Ser	
435 440 445	
gac aac ggg ggc cac ctg gag ccc ctg gac ggg gct gtt cag ctg ggt	1392
Asp Asn Gly Gly His Leu Glu Pro Leu Asp Gly Ala Val Gln Leu Gly	
450 455 460	
ggc tgg aac ggg atc tac aaa ggt ggc aaa gga atg gga gga tgg gaa	1440
Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu	
465 470 475 480	
gga ggt atc cgt gtg cca ggg ata ttc cgg tgg ccg tca gtc ttg gag	1488
Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Ser Val Leu Glu	
485 490 495	
gct ggg aga gtg atc aat gag ccc acc agc tta atg gac atc tat ccg	1536
Ala Gly Arg Val Ile Asn Glu Pro Thr Ser Leu Met Asp Ile Tyr Pro	
500 505 510	
acg ctg tct tat ata ggc gga ggg atc ttg tcc cag gac aga gtg att	1584
Thr Leu Ser Tyr Ile Gly Gly Gly Ile Leu Ser Gln Asp Arg Val Ile	
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gac ggc cag aac cta atg ccc ctg ctg gaa gga agg gcg tcc cac tcc	1632
Asp Gly Gln Asn Leu Met Pro Leu Leu Glu Gly Arg Ala Ser His Ser	
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gac cac gag ttc ctc ttc cac tac tgt ggg gtc tat ctg cac acg gtc	1680
Asp His Glu Phe Leu Phe His Tyr Cys Gly Val Tyr Leu His Thr Val	
545 550 555 560	
agg tgg cat cag aag gac tgt gca act gtg tgg aaa gct cat tat gtg	1728
Arg Trp His Gln Lys Asp Cys Ala Thr Val Trp Lys Ala His Tyr Val	
565 570 575	

act cct aaa ttc tac cct gaa gga aca ggt gcc tgc tat ggg agt gga 1776  
Thr Pro Lys Phe Tyr Pro Glu Gly Thr Gly Ala Cys Tyr Gly Ser Gly  
580 585 590

ata	tgt	tca	tgt	tcg	ggg	gat	gta	acc	tac	cac	gac	cca	cca	ctc	ctc	1824
Ile	Cys	Ser	Cys	Ser	Gly	Asp	Val	Thr	Tyr	His	Asp	Pro	Pro	Leu	Leu	
		595					600					605				

ttt gac atc tca aga gac cct tca gaa gcc ctt cca ctg aac cct gac 1872  
Phe Asp Ile Ser Arg Asp Pro Ser Glu Ala Leu Pro Leu Asn Pro Asp  
610 615 620

aat gag cca tta ttt gac tcc gtg atc aaa aag atg gag gca gcc ata 1920  
Asn Glu Pro Leu Phe Asp Ser Val Ile Lys Lys Met Glu Ala Ala Ile  
625 630 635 640

aga gag cat cgt agg aca cta aca cct gtc cca cag cag ttc tct gtg 1968  
Arg Glu His Arg Arg Thr Leu Thr Pro Val Pro Gln Gln Phe Ser Val  
645 650 655

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Phe Asn Thr Ile Trp Lys Pro Trp Leu Gln Pro Cys Cys Gly Thr Phe  
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ccc ttc tgt ggg tgt gac aag gaa gat gac atc ctt ccc atg gct ccc 2064  
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tga 2067

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Thr Arg Asn Pro Gln Arg Ile Phe Thr Lys His Val Ala Thr Lys Ser  
35 40 45

Ser Ser Ser Lys Cys Gln Leu Asp Gln Gly Gly Lys Ser Leu Val Gln  
50 55 60

Cys Ile Leu Pro Arg Ser Ser Lys Leu Leu Ser Pro Leu Cys Leu Pro  
65 70 75 80

His Pro Cys Gly Ala Leu Leu Leu Tyr Arg Ser Ser Gly Ile Ala Ser  
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Ala Leu Ala Ala Phe Thr Asp Ser Leu Ser Arg Ser Cys Trp Leu Ser  
100 105 110

Val Ser Leu Cys Cys Leu Phe Cys Gly Val Asp Gly Thr Phe Met Thr  
115 120 125

Arg Asn Ala Arg Pro Asn Ile Val Leu Leu Met Ala Asp Asp Leu Gly  
130 135 140

Val Gly Asp Leu Cys Cys Tyr Gly Asn Asn Ser Val Ser Thr Pro Asn  
145 150 155 160

Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala  
165 170 175

Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg  
180 185 190

Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala  
195 200 205

Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr  
210 215 220

Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly  
225 230 235 240

Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr  
245 250 255

His Pro Leu Asn His Gly Phe His Tyr Phe Tyr Gly Val Pro Phe Gly  
260 265 270

Leu Leu Ser Asp Cys Gln Ala Ser Lys Thr Pro Glu Leu His Arg Trp  
275 280 285

Leu Arg Ile Lys Leu Trp Ile Ser Thr Val Ala Leu Ala Leu Val Pro  
290 295 300

Phe Leu Leu Leu Ile Pro Lys Phe Ala Arg Trp Phe Ser Val Pro Trp  
 305 310 315 320

Lys Val Ile Phe Val Phe Ala Leu Leu Ala Phe Leu Phe Phe Thr Ser  
 325 330 335

Trp Tyr Ser Ser Tyr Gly Phe Thr Arg Arg Trp Asn Cys Ile Leu Met  
 340 345 350

Arg Asn His Glu Ile Ile Gln Gln Pro Met Lys Glu Glu Lys Val Ala  
 355 360 365

Ser Leu Met Leu Lys Glu Ala Leu Ala Phe Ile Glu Arg Tyr Lys Arg  
 370 375 380

Glu Pro Phe Leu Leu Phe Phe Ser Phe Leu His Val His Thr Pro Leu  
 385 390 395 400

Ile Ser Lys Lys Lys Phe Val Gly Arg Ser Lys Tyr Gly Arg Tyr Gly  
 405 410 415

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Lys Ile Leu Asp Ala  
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Leu Asp Gln Glu Arg Leu Ala Asn His Thr Leu Val Tyr Phe Thr Ser  
 435 440 445

Asp Asn Gly Gly His Leu Glu Pro Leu Asp Gly Ala Val Gln Leu Gly  
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Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu  
 465 470 475 480

Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Ser Val Leu Glu  
 485 490 495

Ala Gly Arg Val Ile Asn Glu Pro Thr Ser Leu Met Asp Ile Tyr Pro  
 500 505 510

Thr Leu Ser Tyr Ile Gly Gly Gly Ile Leu Ser Gln Asp Arg Val Ile  
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Asp Gly Gln Asn Leu Met Pro Leu Leu Glu Gly Arg Ala Ser His Ser

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Asp His Glu Phe Leu Phe His Tyr Cys Gly Val Tyr Leu His Thr Val  
 545 550 555 560

Arg Trp His Gln Lys Asp Cys Ala Thr Val Trp Lys Ala His Tyr Val  
 565 570 575

Thr Pro Lys Phe Tyr Pro Glu Gly Thr Gly Ala Cys Tyr Gly Ser Gly  
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Ile Cys Ser Cys Ser Gly Asp Val Thr Tyr His Asp Pro Pro Leu Leu  
 595 600 605

Phe Asp Ile Ser Arg Asp Pro Ser Glu Ala Leu Pro Leu Asn Pro Asp  
 610 615 620

Asn Glu Pro Leu Phe Asp Ser Val Ile Lys Lys Met Glu Ala Ala Ile  
 625 630 635 640

Arg Glu His Arg Arg Thr Leu Thr Pro Val Pro Gln Gln Phe Ser Val  
 645 650 655

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Lys Asp Glu Leu

1